

Schreiber, David

From: Swope, Sheridan
 Sent: Saturday, December 04, 2004 5:25 PM
 To: Schreiber, David
 Subject: FW: 09/940,235

Scan this page

David Dearest,

Would you do the following alignments for me?

From 09/940,235:

Align SID 4, residues 1-106 with each of the sequences below:

Align SID 4, residues 150-259 with each of the sequences below:

THANK YOU VERY MUCH!!

Pending Data Base

✓ PCT/US93/09502: SID 1
 ✓ US08/128,299: SID 1

A Geneseq Data Base

✓ AAR10194
 ✓ AAR63120
 ✓ AAY24794
 ✓ AAW94664
 ✓ AAY01556
 ✓ AAY24797

UniProt_02 Data Base

✓ STRP_STREQ

Issued Patents Data Base

✓ US 09/211,542: SID 6 6 2 10 66 7

US 07/549,049 (US 5,240,845) SID 1 & SID 2 & SID 3 ← no biotech data

✓ US 08/560,098: SID 52
 ✓ US 09/211,542: SID 2 & SID 5 → NA
 ✓ US 08/568,393B: SID 1

GenEmbl Data Base

✓ E03308
 ✓ AR143998
 ✓ STRSKC
 ✓ SEDEXB
 ✓ I05204

N GeneSeq Data Base

✓ AAX80492
 ✓ AAX16632
 ✓ AAX80497

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 6, 2004, 15:00:52 ; Search time 2 Seconds
(without alignments)
2.533 Million cell updates/sec

Title: US-09-940-235-4
Perfect score: 600
Sequence: 1 QAQMVPQSPVAVSQSKPG.....SMWDTCTIGAGRGISCTI 106

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 10 seqs, 23900 residues

Total number of hits satisfying chosen parameters: 20

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 20 summaries

Command line parameters:
-MODEL=frame_p2n.model -DEV=soft -O=Pending Patents AA.Main:US-09-940-235-4
-DB= -Suffix=ptc -OUT=align4_1_106_seq -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=106 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=20
-DOALIGN=200 -THR SCORE=ptc -THR MAX=100 -THR MIN=0 -ALIGN=20 -MODE=LOCAL
-OUTFWT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -NCPV=6
-NO_XLPXY -NEG SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	7.5	1262	E03308	ACCESSION:E03308
2	44	7.3	2568	STRSKC	ACCESSION:K02986
3	44	7.3	8931	SEDEXB	ACCESSION:X72832
C 4	43	7.2	1262	E03308	ACCESSION:E03308
5	38	6.3	2385	1	AR143998
C 6	38	6.3	2385	1	AR143998
7	38	6.3	2385	8	AAx80497
C 8	38	6.3	2385	8	AAx80497
C 9	38	6.3	8931	4	SEDEXB
10	33.5	5.6	1242	6	AAx16632
11	33.5	5.6	1242	7	AAx80492

12	33.5	5.6	1242	9	us-09-211-542a-5
13	33.5	5.6	1242	10	us-08-568-393b-1
14	33.5	5.6	1401	3	I05204
C 15	28.5	4.8	1242	6	AAx16632
C 16	28.5	4.8	1242	7	AAx80492
C 17	28.5	4.8	1242	9	us-09-211-542a-5
C 18	28.5	4.8	1242	10	us-08-568-393b-1
C 19	28.5	4.8	1401	3	I05204
C 20	28.5	4.8	2568	5	STRSKC

ACCESSION:I05204
Streptococcus equi
Streptococcus equi
ACCESSION:I05204
ACCESSION:K02986

ALIGNMENTS

RESULT 1
E03308
LOCUS E03308 1262 bp DNA linear PAT 29-SEP-1997
DEFINITION DNA encoding recombinant streptokinase.
ACCESSION E03308
VERSION E03308.1 GI:2171525
KEYWORDS JP 1992011892-A/1.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 1262)
AUTHORS Fujii,S., Katano,T., Majima,E., Ogino,K., Ono,K., Sakata,Y. and Uenoyama,T.
TITLE PROTEIN OF STREPTOKINASES, CORRESPONDING GENE, CORRESPONDING PLASMID RECOMBINANT, CORRESPONDING CHARACTER TRANSFORMANT AND PRODUCTION
JOURNAL Patent: JP 1992011892-A 1 16-JAN-1992;
COMMENT OHSUKA PHARMACEUTICAL INC
OS Artificial gene
OC Artificial sequence; Genes.
PN JP 1992011892-A/1
PD 16-JAN-1992
PF 06-JUL-1990 JP 1990179851
PR 11-JUL-1989 JP 89P 179432, 27-NOV-1989 JP 89P 307957, PR 11-APR-1990 JP 90P 96830
PI FUJII SETSUO, KATANO TAMITAKA, MAJIMA EIJI, OGINO KOICHI, PI ONO KENJI,
PI SAKATA YASUYO, UENOYAMA TSUTOMU
PC C12N15/58,C12N1/21,C12N9/70, (C12N1/21,C12R1:19), (C12N9/70, PC C12R1:19);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: clone=PSKX;
FH Key Location/Qualifiers
FT 5'UTR 1..11
FT CDS 12..1256
FT mat_peptide 12..1253
FT 3'UTR 1257..1263.
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1..1262
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Alignment Scores:
Pred. No.: 0.651 Length: 1262
Score: 45.00 Matches: 22
Percent Similarity: 42.86% Conservative: 11
Best Local Similarity: 28.57% Mismatches: 21
Query Match: 7.50% Indels: 23
DB: 2 Gaps: 6

US-09-940-235-4 (1-259) x E03308 (1-1262)

Qy 6 ValGlnPro-----GlnSerProValAlaValSerGlnSerLysProGlyCysTyrAsp 23

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Db      992 GTACGACCGCGTGACAAAGCTAAACTGCTGTACAACAA-----CCTGGATGCTTT--- 1042
Qy      24  AenGlyLysHisTyrGlnIleAenGlnTrp-----GluArg-ThrTyrLeuGlyAs 41
Db      1043 -----CGGTATCATGAGTACACCTGCTGCTGTAAGTAGAAGACACACCATCAGACAC 1096
Qy      41  nValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysProG1 61
Db      1097 CAACCGTATCATCACCGTATACATGCGCAACGT-----CGGGA 1135
Qy      61  ualaGluGluThrCysPhe-----AspLysTyrThr 71
Db      1136 AGGTGAATAATGCATCTTACCATCTGCGATATGACAAAGACCGTTACACC 1184

RESULT 2
STRSKC          2568 bp      DNA      linear      BCT 26-APR-1993
LOCUS          Streptococcus equisimilis (H46A) streptokinase gene, complete cds.
DEFINITION
ACCESSION      K02986
VERSION        K02986.1 GI:153808
KEYWORDS       Streptokinase.
SOURCE         Streptococcus dysgalactiae subsp. equisimilis
ORGANISM       Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
               Streptococcus.
REFERENCE      1 (bases 1 to 2568)
AUTHORS        Malke,H., Roe,B. and Ferretti,J.J.
TITLE          Nucleotide sequence of the streptokinase gene from Streptococcus
               equisimilis H46A
JOURNAL        Gene 34 (2-3), 357-362 (1985)
MEDLINE        85232082
PUBMED         2989113
COMMENT        Original source text: S.equisimilis (strain H46A) DNA, clone pMF5.
               Draft entry and hard copy of sequence for [1] kindly provided by
               J.J.Ferretti, 03-SEP-1985.
               The -35 and -10 regions are located at positions 760-765 and
               781-786 respectively and an SD sequence at 808-813. Downstream
               from the coding region inverted repeats (positions 2176-2190 and
               2203-2217) are thought to function as transcription terminators.
               The nucleotide sequence of skc does not support the hypothesis that
               the gene has evolved by duplication and fusion, as suggested by
               internal two-fold AA homologies of its product.
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             /db_xref="GI:153808"
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               FLLSGVRVPYKEKPIQNAKSDVDEYVQFTPLNPDFFRPLGKDTLLKTLAIGD
               TITSBLLAQOASILLKNHPGVTIYERDSSIIVTHNDIIFRTILPMDQETRYVRNREQ
               AVRINKSLGEIENNTDILISEKYVYLKKEKPYDFDFRSHLKLFTIKYVDVDTNELL
               KSEQLLTASERNLDFLDYDRDKAKLLYNLDAFGIMDYTLTGKVEDHDDTNRILT
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             819..896
             /note="streptokinase signal peptide"
             897..2138
             /product="streptokinase"

sig_peptide      2.05      Length:      2568
mat_peptide      44.00      Matches:      10
Percent Similarity: 42.86%      Conservative: 8

Alignment Scores:
Pred. No.:      44.00
Score:          42.86%
Percent Similarity: 42.86%

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Best Local Similarity: 23.81%      Mismatches: 14
Query Match:          7.33%      Indels: 10
DB:                   5          Gaps: 1

US-09-940-235-4 (1-259) x STRSKC (1-2568)

Qy      2  AlAGlGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGlyCys 21
Db      319 GCAAGACCTCATATTAGCCCAACCCCACTCAAGTAATAAGCGCTCTT----- 366
Qy      22  TyrAspAsnGlyLysHisTyrGlnIleAsnGlnTrpGluArgThrTyrLeuGlyAsn 41
Db      367 -----TTTCGATAAACATGATTTGGGAAATGACATATATTGGTCCC 408
Qy      42  ValLeu 43
Db      409 CTTCCTT 414

RESULT 3
SEDEXB          8931 bp      DNA      linear      BCT 17-FEB-1997
LOCUS          S.equisimilis dextb, abc, lrp, skc, rel genes and ORF1.
DEFINITION
ACCESSION      X72832
VERSION        X72832.1 GI:407876
KEYWORDS       abc gene; ABC transporter; dextB gene; dextran glucosidase; glucan
               1,6-alpha-glucosidase; leucine rich protein; LRP gene; ORF1; rel
               gene; skc gene; streptokinase; stringent response-like protein.
SOURCE         Streptococcus dysgalactiae subsp. equisimilis
ORGANISM       Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
               Streptococcus.
REFERENCE      1 (bases 3621 to 6190)
AUTHORS        Malke,H., Roe,B. and Ferretti,J.J.
TITLE          Nucleotide sequence of the streptokinase gene from Streptococcus
               equisimilis H46A
JOURNAL        Gene 34 (2-3), 357-362 (1985)
MEDLINE        85232082
PUBMED         2989113
REFERENCE      2 (bases 1 to 4188; 5790 to 8931)
AUTHORS        Mechold,U., Steiner,K., Vettermann,S. and Malke,H.
TITLE          Genetic organization of the streptokinase region of the
               Streptococcus equisimilis H46A chromosome
JOURNAL        Mol. Gen. Genet. 241 (1-2), 129-140 (1993)
MEDLINE        94049672
PUBMED         8232196
REFERENCE      3 (bases 1 to 8931)
AUTHORS        Malke,H.
TITLE          Direct Submission
JOURNAL        Submitted (05-MAY-1993) H. Malke, Institute for Molecular Biology,
               Jena University, Winzerlaer Str 10, 07708 Jena, FRG
COMMENT        Related sequences: K02986, M19346, X13399 & X13400.
FEATURES
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             /strain="H46A"
             /isolate="human group C strain"
             /sub_species="equisimilis"
             /db_xref="taxon:119602"
             /clone_lib="E.coli plasmid library containing subfragments
               of the submitted seq:pSHD14/16, pSPV19, pSH2, pMF1,
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HTSDHFAVEARENPSPERYIWRDEPNNLMSIFSGSAMBLDEASGGYYIHLFPSK
KOPDLNENAHVRQKIYDMNFWIAKGIIGFRMDVLDLTKIPDSITGNGPRLHDYL
KEMNQATFGNHQVMTVGETWGTGATPEIARQYSRPENKELSMVFQFEHVGLQHKENAPKM
DYABLDVPAKATIFSKWOTELKLGWNSLFWNNHDLPRVLSIWNDSIYREKSAKA
LAILLHWRGTPIYVIGEGIGMTNYPKDLTEVDDJESLNYAKEAMENGVPAARVNWS
IRKGRDNARTMQMSKDTAGFSEAQETWLPVNPYQEIINVADALANQDSIFITYQQ
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complement(1780..1810)
/gene="abc"
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complement(2482..2499)
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/codon_start=1
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/product="ABC transporter"
/protein_id="CAA51349.1"
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STLRIMAGLEDISEGLKIDGVEVNDKSPKRDIAWVPONYALPHMTYVDNNAFGL
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/note="(+1) frame shift mutation in H46A"
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/db_xref="Swiss-Prot:Q54087"
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TITSQELLAQAQSIILKNHPGYTIYERDSSIIVTHDNDIFRILPMDQEFTRYVKNRQ
AYRINKSGLEINNTDLISEKYVLLKGEKPYDPFRSHLKLFTIKYVDVDTNELL
KSRQLLTASERNLDFRLYDPRDKALLNNLDAFGIMDYTLTGKVDNDDTNRIT
VYMKRPEGENASYHLAYDKDRYTEEREVYSILRYTGTPIPNPNDK"
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Alignment Scores:
Pred. No.:      8.55      Length:      8931
Score:          44.00      Matches:      10
Percent Similarity: 42.86%      Conservative: 8
Best Local Similarity: 23.81%      Mismatches: 14
Query Match:      7.33%      Indels:      10
DB:              4      Gaps:      1

US-09-940-235-4 (1-259) x SEDEXB (1-8931)

Qy 2 AlaGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGlyCys 21
Db 3939 GCAAGACCTCATATTGACCAACCCACCTCAAGTAATAAGCGTCTT----- 3986
Qy 22 TyrAspAsnGlyLysHisTyrGlnIleAsnGlnTrpGluArgThrTyrLeuGlyAsn 41
Db 3987 -----TTTCGGATAAACATGATTGGGAAAATGCACATATTGGTCCC 4028
Qy 42 ValLeu 43
Db 4029 CTTCCT 4034

RESULT 4
E03308/c
LOCUS E03308 1262 bp DNA linear PAT 29-SEP-1997
DEFINITION DNA encoding recombinant streptokinase.
ACCESSION E03308
VERSION E03308.1 GI:2171525
KEYWORDS JP 1992011892-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 1262)
AUTHORS Fujii,S., Katano,T., Majima,E., Ogino,K., Ono,K., Sakata,Y. and Uenoyama,T.
TITLE PROTEIN OF STREPTOKINASES, CORRESPONDING GENE, CORRESPONDING PLASMID RECOMBINANT, CORRESPONDING CHARACTER TRANSFORMANT AND PRODUCTION
JOURNAL Patent: JP 1992011892-A 1 16-JAN-1992; OTSUKA PHARMACEUT FACTORY INC
COMMENT OS Artificial gene
PN JP 1992011892-A/1
PD 16-JAN-1992
PF 06-JUL-1990 JP 1990179851
PR 11-JUL-1989 JP 89P 179432, 27-NOV-1989 JP 89P 307957, PR 11-APR-1990 JP 90P 96830
PI FUJII SETSUO, KATANO TAMITAKA, MAJIMA EIJI, OGINO KOICHI, PI ONO KENJI,
PI SAKATA YASUYO, UENOYAMA TSUTOMU
PC C12N15/58,C12N1/21,C12N9/70,(C12N1/21,C12R1:19),(C12N9/70, PC C12R1:19);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: clone=PSKX;
FH Key Location/Qualifiers
FT 5'UTR 1..11
FT CDS 12..1256
FT mat_peptide 12..1253
FT 3'UTR 1257..1263.
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Alignment Scores:
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Score:          43.00      Matches:      12
Percent Similarity: 40.30%      Conservative: 15
Best Local Similarity: 17.91%      Mismatches: 26
Query Match:      7.17%      Indels:      14
DB:              2      Gaps:      1

US-09-940-235-4 (1-259) x E03308 (1-1262)

Qy 36 ArgThrTyrLeuGlyAsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsn 55
Db 293 AGAATGTACCTTACCGCATCGCTGTTCTCGATTGCTTT----- 255
Qy 56 CysGlnSerLysProGluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyr 75
Db 254 -----CAGCAGATCTGCTTCTCGATTATGAGACATAGCGCC 216
Qy 76 ArgValGlyAspThrTyrGluArgProLysAspSerMetIleTrpAspCysThrCysIle 95
Db 215 AGAGTCAGTAGCGAACGGTTTAGATTTCGGGGACAGCCCTGTCGGGTTTACCACCATG 156
Qy 96 GlyAlaGlyArgGlyArgIle 102
Db 155 GCGCGGACGAGAGTCAGGTC 135

RESULT 5
AR143998
LOCUS AR143998 2385 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6210667.
ACCESSION AR143998
VERSION AR143998.1 GI:15105865
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2385)
AUTHORS Reed,G.L.
TITLE Bacterial fibrin-dependent plasminogen activator
JOURNAL Patent: US 6210667-A 1 03-APR-2001;
FEATURES Location/Qualifiers
source
1..2385
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Alignment Scores:
Pred. No.:      7.15      Length:      2385
Score:          38.00      Matches:      15
Percent Similarity: 33.90%      Conservative: 5
Best Local Similarity: 25.42%      Mismatches: 35
Query Match:      6.33%      Indels:      4
DB:              1      Gaps:      1

US-09-940-235-4 (1-259) x AR143998 (1-2385)

Qy 14 ValSerGlnSerLysProGlyCysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGln 33
Db 933 GTTGGCGAAGATCCACGATTTCGCCACCATGGAAGAACGCCAGAAAGGTGAATCAT 992
Qy 34 TrpGluArgThrTyrLeuGlyAsnValLeuValCysThrCysTyrGlyGly----- 50
Db 993 GCCGAACATCCGCGAGATGCGGCTTTCTGTATCGCGTACTCGGTGATCAACGC 1052
Qy 51 ---SerArgGlyPheAsnCysGlnSerLysProGluAlaGluGluThrCysPheAsp 68
Db 1053 CGCCAGCGGTTCGTGACACTGTCGATGAAGCCCTGAAAGACGCGCAGAGACTAATTCGAG 1109

RESULT 6
AR143998/c
LOCUS AR143998 2385 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6210667.
ACCESSION AR143998
VERSION AR143998.1 GI:15105865
```

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2385)

AUTHORS Reed,G.L.

TITLE Bacterial fibrin-dependent plasminogen activator

JOURNAL Patent: US 6210667-A 1 03-APR-2001;

FEATURES Location/Qualifiers

source 1..2385

/organism="unknown"

/mol_type="unassigned DNA"

Alignment Scores:

Pred. No.: 7.15 Length: 2385
 Score: 38.00 Matches: 11
 Percent Similarity: 38.89% Conservative: 3
 Best Local Similarity: 30.56% Mismatches: 22
 Query Match: 6.33% Indels: 0
 DB: 1 Gaps: 0

US-09-940-235-4 (1-259) x AR143998 (1-2385)

Qy 1 GlnAlaGlnGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20

Db 1156 CAGGTCCAGCAATCCTACCCCTCGATGGATCCCGCGGGGTACCGAGCTCGAATTAGTCT 1097

Qy 21 CysTyrAspAsnGlyHisTyrGlnIleAsnGlnGlnTrpGluArg 36

Db 1096 GCGCGTCTTCAGGGCTTCATCGACAGTCTGACCCGCTGGCGGCGT 1049

RESULT 7

AAX80497

ID AAX80497 standard; cDNA; 2385 BP.

XX AC AAX80497;

XX DT 26-AUG-1999 (first entry)

XX DE Streptokinase and maltose binding protein fusion protein encoding cDNA.

XX KW Streptococcus; streptokinase; fibrin-dependent plasminogen activator;

XX KW nSK; rSK; bacterial; blood clot; thrombotic condition;

XX KW myocardial infarction; venous thrombosis; pulmonary embolism;

XX KW cerebral thrombosis; graft thrombosis; arterial thrombosis; ss.

XX OS Streptococcus dysgalactiae subsp. equisimilis.

XX OS Synthetic.

XX PN WO9931247-A1.

XX PD 24-JUN-1999.

XX PF 15-DEC-1998; 98WO-US026694.

XX PR 15-DEC-1997; 97US-0069497P.

XX PA (HARD) HARVARD COLLEGE.

XX PI Reed GL;

XX DR WPI; 1999-395183/33.

XX DR P-PSDB; AAY24797.

XX PT N-terminally deleted streptokinase.

XX PS Example; Page 45-48; 73pp; English.

XX CC The present invention describes an isolated bacterial protein that

XX CC induces fibrin-dependent plasminogen activation in a pharmaceutical

XX CC composition for dissolving blood clots. Also described are: (1) a

XX CC composition comprising an isolated modified streptokinase, the

XX CC modification being removal of amino acid residues in the amino terminus;

CC (2) a method for dissolving a blood clot in a subject, comprising
 CC administering to the subject a fibrin-dependent streptokinase protein; a
 CC nucleic acid (1) encoding a modified bacterial streptokinase; (3) an
 CC expression vector comprising (1); and (4) a host cell transformed with
 CC the expression vector of (3). The pharmaceutical composition comprising a
 CC bacterial fibrin-dependent plasminogen activator is useful for dissolving
 CC blood clots in patients with a thrombotic condition, e.g. myocardial
 CC infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis,
 CC graft thrombosis and arterial thrombosis. The modified streptokinase can
 CC also be used in non-human mammals. Streptokinase activation of
 CC plasminogen is at least 10-fold, preferably 100-fold greater in the
 CC presence of fibrin than in the absence of fibrin. The modified
 CC streptokinase has at least one amino acid substitution that inactivates a
 CC substrate site for proteolytic cleavage. This reduces the rate of
 CC degradation of the streptokinase at least two-fold. The present sequence
 CC encodes a streptokinase and maltose binding protein fusion protein from
 CC an example of the present invention
 XX SQ Sequence 2385 BP; 745 A; 547 C; 549 G; 544 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 7.15 Length: 2385
 Score: 38.00 Matches: 15
 Percent Similarity: 33.90% Conservative: 5
 Best Local Similarity: 25.42% Mismatches: 35
 Query Match: 6.33% Indels: 4
 DB: 8 Gaps: 1

US-09-940-235-4 (1-259) x AAX80497 (1-2385)

Qy 14 ValSerGlnSerLysProGlyCysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGln 33

Db 933 GTTGGCGAAAGATCCACGTATTGCCGCCACCATGGAAGCCAGAAAGGTGAATCAT 992

Qy 34 TrpGluArgThrTyrLeuGlyAsnValLeuValCysThrCysTyrGlyGly----- 50

Db 993 GCGAACAATCCCGCAGATGCCCTTTCTGGTATGCCGTGCTACTCGGTGATCAACGC 1052

Qy 51 ---SerArgGlyPheAsnCysGluSerLysProGluAlaGluGluThrCysPheAsp 68

Db 1053 CGCCAGCGTGTGCAGACTGTGATGAAGCCCTGAAGCGCGCAGACTAATTCGAG 1109

RESULT 8

AAX80497/c

ID AAX80497 standard; cDNA; 2385 BP.

XX AC AAX80497;

XX DT 26-AUG-1999 (first entry)

XX DE Streptokinase and maltose binding protein fusion protein encoding cDNA.

XX KW Streptococcus; streptokinase; fibrin-dependent plasminogen activator;

XX KW nSK; rSK; bacterial; blood clot; thrombotic condition;

XX KW myocardial infarction; venous thrombosis; pulmonary embolism;

XX KW cerebral thrombosis; graft thrombosis; arterial thrombosis; ss.

XX OS Streptococcus dysgalactiae subsp. equisimilis.

XX OS Synthetic.

XX PN WO9931247-A1.

XX PD 24-JUN-1999.

XX PF 15-DEC-1998; 98WO-US026694.

XX PR 15-DEC-1997; 97US-0069497P.

XX PA (HARD) HARVARD COLLEGE.

XX PI Reed GL;

XX XX WPI; 1999-395183/33.

```

DR P-PSDB; AAY24797.
XX
PT N-terminally deleted streptokinase.
PS
PS Example; Page 45-48; 73pp; English.
XX
CC The present invention describes an isolated bacterial protein that
CC induces fibrin-dependent plasminogen activation in a pharmaceutical
CC composition for dissolving blood clots. Also described are: (1) a
CC composition comprising an isolated modified streptokinase, the
CC modification being removal of amino acid residues in the amino terminus;
CC (2) a method for dissolving a blood clot in a subject, comprising
CC administering to the subject a fibrin-dependent streptokinase protein; a
CC nucleic acid (1) encoding a modified bacterial streptokinase; (3) an
CC expression vector comprising (1); and (4) a host cell transformed with
CC the expression vector of (3). The pharmaceutical composition comprising a
CC bacterial fibrin-dependent plasminogen activator is useful for dissolving
CC blood clots in patients with a thrombotic condition, e.g. myocardial
CC infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis,
CC graft thrombosis and arterial thrombosis. The modified streptokinase can
CC also be used in non-human mammals. Streptokinase activation of
CC plasminogen is at least 10-fold, preferably 100-fold greater in the
CC presence of fibrin than in the absence of fibrin. The modified
CC streptokinase has at least one amino acid substitution that inactivates a
CC substrate site for proteolytic cleavage. This reduces the rate of
CC degradation of the streptokinase at least two-fold. The present sequence
CC encodes a streptokinase and maltose binding protein fusion protein from
CC an example of the present invention
XX
SQ Sequence 2385 BP; 745 A; 547 C; 549 G; 544 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 7.15 Length: 2385
Score: 38.00 Matches: 11
Percent Similarity: 38.89% Conservative: 3
Best Local Similarity: 30.56% Mismatches: 22
Query Match: 6.33% Indels: 0
DB: 8 Gaps: 0

US-09-940-235-4 (1-259) x AAY80497 (1-2385)

QY 1 GlnAlaGlnMetValGlnProGlnSerProValaValSerGlnSerLysProGly 20
Db 1156 CAGGTCACAGATCTCTACCTCGATGATCCCGCGCGGTACCGAGTCGAATTAGTCT 1097
QY 21 CysTyrAspAsnGlyHisTyrGlnIleAsnGlnTrpGluArg 36
Db 1096 GCGCGCTCTTTCAGGGCTTCATCGACAGTCTGACGACCGTGGCGCGGT 1049

RESULT 9
SEDEX/c SEDEXB 8931 bp DNA linear BCT 17-FEB-1997
LOCUS S.equisimilis dextb, abc, lrp, skc, rel genes and ORF1.
DEFINITION X72832
ACCESSION X72832
VERSION X72832.1 GI:407876
KEYWORDS abc gene; ABC transporter; dextB gene; dextran glucosidase; glucan
1,6-alpha-glucosidase; leucine rich protein; LRP gene; ORF1; rel
gene; skc gene; streptokinase; stringent response-like protein.
SOURCE Streptococcus dysgalactiae subsp. equisimilis
ORGANISM Streptococcus dysgalactiae subsp. equisimilis
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus
REFERENCE 1 (bases 3621 to 6190)
AUTHORS Malke,H., Roe,B. and Ferretti,J.J.
TITLE Nucleotide sequence of the streptokinase gene from Streptococcus
equisimilis H46A
JOURNAL Gene 34 (2-3), 357-362 (1985)
MEDLINE 85232082
PUBMED 2989113
REFERENCE 2 (bases 1 to 4188; 5790 to 8931)
AUTHORS Mechold,U., Steiner,K., Vettermann,S. and Malke,H.
TITLE Genetic organization of the streptokinase region of the
Streptococcus equisimilis H46A chromosome

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JOURNAL Mol. Gen. Genet. 241 (1-2), 129-140 (1993)
MEDLINE 94049672
PUBMED 8232196
REFERENCE 3 (bases 1 to 8931)
AUTHORS Malke,H.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-1993) H. Malke, Institute for Molecular Biology,
Jena University, Winzerlaer Str 10, 07708 Jena, FRG
COMMENT Related sequences: K02986, M19346, X13399 & X13400.
FEATURES
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            IRKVGDRNARTPMWSKTHAGSEAQETLWLPVNPYQELNVADALANODSIFVTYQQ
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          /note="TG motif"
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          Pred. No.: 18.4          Length: 8931
          Score: 38.00          Matches: 9
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          Best Local Similarity: 42.86%          Mismatches: 12
          Query Match: 6.33%          Indels: 0
          DB: 4          Gaps: 0
          US-09-940-235-4 (1-259) x SEDEXB (1-8931)
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          Db 7870 ACCAAATCAAGTCTTATACCACTGACCAAGGCTTGTGGTGTGTTATGTCGACCA 7811
          QY 85 Lys 85
          Db 7810 AAA 7808
          RESULT 10
          AAX16632
          ID AAX16632 standard; DNA; 1242 BP.
          XX
          AC AAX16632;
          XX
          DT 17-OCT-2003 (revised)
          DT 04-MAY-1999 (first entry)
          XX
          DE Streptococcus equisimilis native streptokinase encoding DNA.
          XX
          KW Streptococcus equisimilis H46A; streptokinase; mutant; fibrinolytic;
          KW plasma clot; hydrolysis; haemolytic Streptococcus; plasminogen; plasmin;
          KW serine protease; fibrin; blood clot; thrombolytic;
          KW vascular thromboembolytic symptom; acute myocardial infarction;
          KW fibrinolysis; resistance; ds.
          XX
          OS Streptococcus dysgalactiae subsp. equisimilis.
          XX
          FH Key Location/Qualifiers
          FT CDS 1..1242
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PN      US5876999-A.
XX
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PD      02-MAR-1999.
XX
XX
PF      06-DEC-1995; 95US-00568393.
XX
XX
PR      06-DEC-1995; 95US-00568393.
XX
XX
PA      (NASC-) NAT SCI COUNCIL.
XX
PI      Wu H;
XX
DR      WPI; 1999-189643/16.
XX
DR      P-PSDB; AAW94664.
XX
XX
XX      Mutant streptokinase polypeptide - useful as plasmin-resistant
XX      thrombolytic agent.
XX
PS      Claim 1; Col 7-10; 17pp; English.
XX
XX      The present invention describes a mutant streptokinase (SK) polypeptide
CC      in which at least one of the amino acids in the Pro58-Lys59-Ser60-Lys61
CC      segment of the corresponding native SK is replaced by another amino acid.
CC      The present sequence encodes native SK. SK is a secretory protein of
CC      haemolytic Streptococcus able to activate human plasminogen (HPLg) to
CC      plasmin (HPLm), which is a serine protease able to catalyse the
CC      hydrolysis of fibrin in blood clots. The SK is useful as a thrombolytic
CC      agent in the treatment of vascular thromboembolytic symptoms such as
CC      acute myocardial infarction. Compared with wild-type SK, the K59E mutant
CC      is more resistant to degradation by human plasmin and is more effective
CC      both in acting as a fibrinolytic agent and in activating human plasminogen.
CC      (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ      Sequence 1242 BP; 423 A; 268 C; 237 G; 314 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      8.8      Length:      1242
Score:          33.50    Matches:      10
Percent Similarity: 38.24% Conservative: 3
Best Local Similarity: 29.41% Mismatches: 8
Query Match:     5.58% Indels:      13
DB:              6      Gaps:       2

US-09-940-235-4 (1-259) x AAX16632 (1-1242)
QY      44 ValCysThrCysTyrGlySerArgGlyPheAsnCysGluSerLysProGluAlaGlu 63
DB      1090 ATCATACCGTTTATATGGCAAGCGA-----CCCGAGGAGAG 1128
QY      64 GluThrCysPhe-----AspLysTyrThr 71
DB      1129 AATGCTAGCTATCATTTAGCCTATGATATAAGATCGTTATACC 1170

RESULT 11
AAX80492
ID      AAX80492 standard; cDNA; 1242 BP.
XX
XX      AAX80492;
XX
XX      17-OCT-2003 (revised)
XX      26-AUG-1999 (first entry)
XX
XX      Streptococcus equisimilis native streptokinase encoding cDNA.
XX
XX      Streptococcus streptokinase; fibrin-dependent plasminogen activator;
XX      NSK; rSK; bacterial; blood clot; thrombotic condition;
XX      myocardial infarction; venous thrombosis; pulmonary embolism;
XX      cerebral thrombosis; graft thrombosis; arterial thrombosis; ss.
XX      Streptococcus dysgalactiae subsp. equisimilis.

XX      WO9931247-A1.
XX
XX      24-JUN-1999.
XX
XX      15-DEC-1998; 98WO-US026694.
XX
XX      15-DEC-1997; 97US-0069497P.
XX
XX      (HARD ) HARVARD COLLEGE.
XX
XX      Reed GL;
XX
XX      WPI; 1999-395183/33.
XX
XX      P-PSDB; AAY24794.
XX
XX      N-terminally deleted streptokinase.
XX
XX      Claim 44; Page 58-60; 73pp; English.
XX
XX      The present invention describes an isolated bacterial protein that
CC      induces fibrin-dependent plasminogen activation in a pharmaceutical
CC      composition for dissolving blood clots. Also described are: (1) a
CC      composition comprising an isolated modified streptokinase, the
CC      modification being removal of amino acid residues in the amino terminus;
CC      (2) a method for dissolving a blood clot in a subject, comprising
CC      administering to the subject a fibrin-dependent streptokinase protein; a
CC      nucleic acid (1) encoding a modified bacterial streptokinase; (3) an
CC      expression vector comprising (1); and (4) a host cell transformed with
CC      the expression vector of (3). The pharmaceutical composition comprising a
CC      bacterial fibrin-dependent plasminogen activator is useful for dissolving
CC      blood clots in patients with a thrombotic condition, e.g. myocardial
CC      infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis,
CC      graft thrombosis and arterial thrombosis. The modified streptokinase can
CC      also be used in non-human mammals. Streptokinase activation of
CC      plasminogen is at least 10-fold, preferably 100-fold greater in the
CC      presence of fibrin than in the absence of fibrin. The modified
CC      streptokinase has at least one amino acid substitution that inactivates a
CC      substrate site for proteolytic cleavage. This reduces the rate of
CC      degradation of the streptokinase at least two-fold. The present sequence
CC      encodes native streptokinase (nSK). (Updated on 17-OCT-2003 to
XX      standardise OS field)
XX
SQ      Sequence 1242 BP; 424 A; 267 C; 237 G; 314 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      8.8      Length:      1242
Score:          33.50    Matches:      10
Percent Similarity: 38.24% Conservative: 3
Best Local Similarity: 29.41% Mismatches: 8
Query Match:     5.58% Indels:      13
DB:              7      Gaps:       2

US-09-940-235-4 (1-259) x AAX80492 (1-1242)
QY      44 ValCysThrCysTyrGlySerArgGlyPheAsnCysGluSerLysProGluAlaGlu 63
DB      1090 ATCATACCGTTTATATGGCAAGCGA-----CCCGAGGAGAG 1128
QY      64 GluThrCysPhe-----AspLysTyrThr 71
DB      1129 AATGCTAGCTATCATTTAGCCTATGATATAAGATCGTTATACC 1170

RESULT 12
us-09-211-542a-5
XX
XX      Alignment Scores:
XX      Pred. No.:      8.8      Length:      1242
XX      Score:          33.50    Matches:      10
XX      Percent Similarity: 38.24% Conservative: 3
XX      Best Local Similarity: 29.41% Mismatches: 8
XX      Query Match:     5.58% Indels:      13
XX      DB:              9      Gaps:       2

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US-09-940-235-4 (1-259) x us-09-211-542a-5 (1-1242)
Qy 44 ValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysProGluAlaGlu 63
Db 1090 ATCATAAACCGTTTATATGGCAAGCGA-----CCCCGAAGGAGAG 1128

Qy 64 GluThrCysPhe-----AspLysTyrThr 71
Db 1129 AATGCTAGCTATCATTTAGCCTATGATATAAAGATCGTTATACC 1170

RESULT 13
us-08-568-393b-1
Alignment Scores:
Pred. No.: 8-8 Length: 1242
Score: 33.50 Matches: 10
Percent Similarity: 38.24% Conservative: 3
Best Local Similarity: 29.41% Mismatches: 8
Query Match: 5.58% Indels: 13
DB: 10 Gaps: 2

US-09-940-235-4 (1-259) x us-08-568-393b-1 (1-1242)
Qy 44 ValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysProGluAlaGlu 63
Db 1090 ATCATAAACCGTTTATATGGCAAGCGA-----CCCCGAAGGAGAG 1128

Qy 64 GluThrCysPhe-----AspLysTyrThr 71
Db 1129 AATGCTAGCTATCATTTAGCCTATGATATAAAGATCGTTATACC 1170

RESULT 14
I05204
LOCUS I05204 1401 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 5 from Patent EP 0248227.
ACCESSION I05204
VERSION I05204.1 GI:591209
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1401)
AUTHORS Hagenson,M.J. and Stroman,D.W.
TITLE Yeast production of streptokinase
JOURNAL Patent: EP 0248227-A1 5 09-DEC-1987;
FEATURES
source
1. .1401
/mol_type="unassigned DNA"

Alignment Scores:
Pred. No.: 9-86 Length: 1401
Score: 33.50 Matches: 10
Percent Similarity: 38.24% Conservative: 3
Best Local Similarity: 29.41% Mismatches: 8
Query Match: 5.58% Indels: 13
DB: 3 Gaps: 2

US-09-940-235-4 (1-259) x I05204 (1-1401)
Qy 44 ValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysProGluAlaGlu 63
Db 1099 ATCATAAACCGTTTATATGGCAAGCGA-----CCCCGAAGGAGAG 1137

Qy 64 GluThrCysPhe-----AspLysTyrThr 71
Db 1138 AATGTCAGCTATCATTTAGCCTATGATATAAAGATCGTTATACC 1179

RESULT 15
AAAX16632/c
ID AAAX16632 standard; DNA; 1242 BP.
XX
```

```
AC AAAX16632;
XX
DT 17-OCT-2003 (revised)
DT 04-MAY-1999 (first entry)
XX
DE Streptococcus equisimilis native streptokinase encoding DNA.
XX
KW Streptococcus equisimilis H46A; streptokinase; mutant; fibrinolytic;
KW plasma clot; hydrolysis; haemolytic Streptococcus; plasminogen; plasmin;
KW serine protease; fibrin; blood clot; thrombolytic;
KW vascular thromboembolytic symptom; acute myocardial infarction;
KW fibrinolysis; resistance; ds.
XX
OS Streptococcus dysgalactiae subsp. equisimilis.
XX
FH Key Location/Qualifiers
FT CDS 1..1242
FT /*tag= a
FT /transl_except= (pos:40..42,aa:Asn)
FT /note= "no stop codon given"
XX
PN US5876999-A.
XX
PD 02-MAR-1999.
XX
PF 06-DEC-1995; 9SUS-00568393.
XX
PR 06-DEC-1995; 9SUS-00568393.
XX
PA (NASC-) NAT SCI COUNCIL.
XX
PI Wu H;
XX
WPI: 1999-189643/16.
P-PSDB; AAW94664.
XX
PT Mutant streptokinase polypeptide - useful as plasmin-resistant
PT thrombolytic agent.
XX
PS Claim 1; Col 7-10; 17pp; English.
XX
CC The present invention describes a mutant streptokinase (SK) polypeptide
CC in which at least one of the amino acids in the Pro58-Lys59-Ser60-Lys61
CC segment of the corresponding native SK is replaced by another amino acid.
CC The present sequence encodes native SK. SK is a secretory protein of
CC haemolytic Streptococcus able to activate human plasminogen (HPLg) to
CC plasmin (HPLm), which is a serine protease able to catalyse the
CC hydrolysis of fibrin in blood clots. The SK is useful as a thrombolytic
CC agent in the treatment of vascular thromboembolytic symptoms such as
CC acute myocardial infarction. Compared with wild-type SK, the K59E mutant
CC is more resistant to degradation by human plasmin and is more effective
CC both in acting as a fibrinolytic agent and in activating human plasminogen.
CC (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 1242 BP; 423 A; 268 C; 237 G; 314 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 17.4 Length: 1242
Score: 28.50 Matches: 12
Percent Similarity: 34.62% Conservative: 6
Best Local Similarity: 23.08% Mismatches: 19
Query Match: 4.75% Indels: 15
DB: 6 Gaps: 2

US-09-940-235-4 (1-259) x AAAX16632 (1-1242)
Qy 5 MetValGlnProGlnSerProVal-----AlaValSerGlnSerLysProGlyCysTyr 22
Db 581 ATGGTGTACCGATAGTAGTGTGTTTCAATAGTCTTTGAGACCTGGTCTGAAA 522

Qy 23 AspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThrTyrLeuGlyAsnVal 42
Db 521 TCGTCATCAGGGTTTAAGGGAGTAAC----- 495
```

QY 43 LeuValCysThrCysTyrGlyGlySerArgGlyPhe 54
D 54
D 494 -----TGTACAGTATATCCACATCAACAGATTTC 465

RESULT 16

ID AAX80492/c
XX AAX80492 standard; cDNA; 1242 BP.

AC AAX80492;

XX 17-OCT-2003 (revised)

DT 26-AUG-1999 (first entry)

XX Streptococcus equisimilis native streptokinase encoding cDNA.

XX Streptococcus; streptokinase; fibrin-dependent plasminogen activator;
KW nSK; rSK; bacterial; blood clot; thrombotic condition;
KW myocardial infarction; venous thrombosis; pulmonary embolism;
KW cerebral thrombosis; graft thrombosis; arterial thrombosis; ss.

XX Streptococcus dysgalactiae subsp. equisimilis.

XX WO9931247-A1.

XX 24-JUN-1999.

XX 15-DEC-1998; 98WO-US026694.

XX 15-DEC-1997; 97US-0069497P.

XX (HARD) HARVARD COLLEGE.

XX Reed GL;

XX WPI; 1999-395183/33.

DR P-PSDB; AAY24794.

XX N-terminally deleted streptokinase.

XX Claim 44; Page 58-60; 73pp; English.

XX The present invention describes an isolated bacterial protein that
CC induces fibrin-dependent plasminogen activation in a pharmaceutical
CC composition for dissolving blood clots. Also described are: (1) a
CC composition comprising an isolated modified streptokinase, the
CC modification being removal of amino acid residues in the amino terminus;
CC (2) a method for dissolving a blood clot in a subject, comprising
CC administering to the subject a fibrin-dependent streptokinase protein; a
CC nucleic acid (1) encoding a modified bacterial streptokinase; (3) an
CC expression vector comprising (1); and (4) a host cell transformed with
CC the expression vector of (3). The pharmaceutical composition comprising a
CC bacterial fibrin-dependent plasminogen activator is useful for dissolving
CC blood clots in patients with a thrombotic condition, e.g. myocardial
CC infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis,
CC graft thrombosis and arterial thrombosis. The modified streptokinase can
CC also be used in non-human mammals. Streptokinase activation of
CC plasminogen is at least 10-fold, preferably 100-fold greater in the
CC presence of fibrin than in the absence of fibrin. The modified
CC streptokinase has at least one amino acid substitution that inactivates a
CC substrate site for proteolytic cleavage. This reduces the rate of
CC degradation of the streptokinase at least two-fold. The present sequence
CC encodes native streptokinase (nSK). (Updated on 17-OCT-2003 to
CC standardise OS field)

XX Sequence 1242 BP; 424 A; 267 C; 237 G; 314 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 17.4 Length: 1242
Score: 28.50 Matches: 12
Percent Similarity: 34.62% Conservative: 6
Best Local Similarity: 23.08% Mismatches: 19
Query Match: 4.75% Indels: 15

DB: 7 Gaps: 2

US-09-940-235-4 (1-259) x AAX80492 (1-1242)

QY 5 MetValGlnProGlnSerProVal-----AlaValSerGlnSerLysProGlyCysTyr 22
D 54
D 581 ATGGTGTCCCGATAGCTAGTGTTCATATAGCTTCTTTGAGACCTGGTCTGAAA 522

QY 23 AspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThrTyrLeuGlyAsnVal 42
D 521 TCCTCATCAGGGTTTAAGGGAGTAAAC----- 495

QY 43 LeuValCysThrCysTyrGlyGlySerArgGlyPhe 54
D 494 -----TGTACAGTATATCCACATCAACAGATTTC 465

RESULT 17

us-09-211-542a-5/c

Alignment Scores:

Pred. No.: 17.4 Length: 1242
Score: 28.50 Matches: 12
Percent Similarity: 34.62% Conservative: 6
Best Local Similarity: 23.08% Mismatches: 19
Query Match: 4.75% Indels: 15
DB: 9 Gaps: 2

US-09-940-235-4 (1-259) x us-09-211-542a-5 (1-1242)

QY 5 MetValGlnProGlnSerProVal-----AlaValSerGlnSerLysProGlyCysTyr 22
D 581 ATGGTGTCCCGATAGCTAGTGTTCATATAGCTTCTTTGAGACCTGGTCTGAAA 522

QY 23 AspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThrTyrLeuGlyAsnVal 42
D 521 TCCTCATCAGGGTTTAAGGGAGTAAAC----- 495

QY 43 LeuValCysThrCysTyrGlyGlySerArgGlyPhe 54
D 494 -----TGTACAGTATATCCACATCAACAGATTTC 465

RESULT 18

us-08-568-393b-1/c

Alignment Scores:

Pred. No.: 17.4 Length: 1242
Score: 28.50 Matches: 12
Percent Similarity: 34.62% Conservative: 6
Best Local Similarity: 23.08% Mismatches: 19
Query Match: 4.75% Indels: 15
DB: 10 Gaps: 2

US-09-940-235-4 (1-259) x us-08-568-393b-1 (1-1242)

QY 5 MetValGlnProGlnSerProVal-----AlaValSerGlnSerLysProGlyCysTyr 22
D 581 ATGGTGTCCCGATAGCTAGTGTTCATATAGCTTCTTTGAGACCTGGTCTGAAA 522

QY 23 AspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThrTyrLeuGlyAsnVal 42
D 521 TCCTCATCAGGGTTTAAGGGAGTAAAC----- 495

QY 43 LeuValCysThrCysTyrGlyGlySerArgGlyPhe 54
D 494 -----TGTACAGTATATCCACATCAACAGATTTC 465

RESULT 19

I05204/c

LOCUS I05204 1401 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 5 from Patent EP 0248227.
ACCESSION I05204
VERSION I05204.1 GI:591209
KEYWORDS

```

SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 1401)
AUTHORS     Hagenson,M.J. and Stroman,D.W.
TITLE       Yeast production of streptokinase
JOURNAL     Patent: EP 0248227-A1 5 09-DEC-1987;
FEATURES    Location/Qualifiers
             source
               1..1401
               /organism="unknown"
               /mol_type="unassigned DNA"

Alignment Scores:
Pred. No.:      18.1      Length:      1401
Score:          28.50     Matches:      12
Percent Similarity: 34.62% Conservative: 6
Best Local Similarity: 23.08% Mismatches: 19
Query Match:    4.75%     Indels:      15
DB:             3        Gaps:         2

US-09-940-235-4 (1-259) x I05204 (1-1401)

Qy      5 MetValGlnProGlnSerProVal-----AlaValSerGlnSerLysProGlyCysTyr 22
Db      590 ATGGTGTACCCGATAGCTAGTGTTCATATAGCTTAGTATCTTTGAGACCTGGTCTGAAA 531
Qy      23 AspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThrTyrLeuGlyAsnVal 42
Db      530 TCGTCATCAGGGTTTAAGGGAGTAAAC-----
Qy      43 LeuValCysThrCysTyrGlyGlySerArgGlyPhe 54
Db      503 -----TGTACAGTATATTCACATCAACAGATTTC 474

RESULT 20
STRSKC/c  LOCUS
DEFINITION Streptococcus equisimilis (H46A) streptokinase gene, complete cds.
ACCESSION K02986
VERSION   K02986.1 GI:153808
KEYWORDS  streptokinase.
SOURCE    Streptococcus dysgalactiae subsp. equisimilis
ORGANISM  Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
           Streptococcus.
REFERENCE 1 (bases 1 to 2568)
AUTHORS   Malke,H., Roe,B. and Ferretti,J.J.
TITLE     Nucleotide sequence of the streptokinase gene from Streptococcus equisimilis H46A
JOURNAL   Gene 34 (2-3), 357-362 (1985)
MEDLINE   85232082
PUBMED    2989113
COMMENT   Original source text: S.equisimilis (strain H46A) DNA, clone pMF5.
           Draft entry and hard copy of sequence for [1] kindly provided by
           J.J.Ferretti, 03-SEP-1985.
           The -35 and -10 regions are located at positions 760-765 and
           781-786 respectively and an SD sequence at 808-813. Downstream
           from the coding region inverted repeats (positions 2176-2190 and
           2203-2217) are thought to function as transcription terminators.
           The nucleotide sequence of skc does not support the hypothesis that
           the gene has evolved by duplication and fusion, as suggested by
           internal two-fold AA homologies of its product.

FEATURES    Location/Qualifiers
             source
               1..2568
               /organism="Streptococcus dysgalactiae subsp. equisimilis"
               /mol_type="genomic DNA"
               /db_xref="taxon:119602"
               794..>2141
               /product="skc mRNA"
               819..2141
               /notes="prestreptokinase"
               /codon_start=1
               /transl_table=11

sig_peptide 819..896
mat_peptide 897..2138
/product="streptokinase"

Alignment Scores:
Pred. No.:      19.9      Length:      2568
Score:          28.50     Matches:      12
Percent Similarity: 34.62% Conservative: 6
Best Local Similarity: 23.08% Mismatches: 19
Query Match:    4.75%     Indels:      15
DB:             5        Gaps:         2

US-09-940-235-4 (1-259) x STRSKC (1-2568)

Qy      5 MetValGlnProGlnSerProVal-----AlaValSerGlnSerLysProGlyCysTyr 22
Db      1477 ATGGTGTACCCGATAGCTAGTGTTCATATAGCTTAGTATCTTTGAGACCTGGTCTGAAA 1418
Qy      23 AspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThrTyrLeuGlyAsnVal 42
Db      1417 TCGTCATCAGGGTTTAAGGGAGTAAAC-----
Qy      43 LeuValCysThrCysTyrGlyGlySerArgGlyPhe 54
Db      1390 -----TGTACAGTATATTCACATCAACAGATTTC 1361

Search completed: December 6, 2004, 15:00:58
Job time : 5 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 6, 2004, 14:53:42 ; Search time 1 Seconds
(without alignments)
0.613 Million cell updates/sec

Title: US-09-940-235-4
Perfect score: 500
Sequence: 1 QAQWVQPSPVAVSQKPG.....SMIWDCTCIGAGRGISCTI 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 12 seqs, 5782 residues

Total number of hits satisfying chosen parameters: 12

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 12 summaries

Database :
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2: /staff_overflow/sdavid-tmp/dec04/swope235/pep/aar63120.geneseqp1990a
3: /staff_overflow/sdavid-tmp/dec04/swope235/pep/aaw94664.geneseqp1990a
4: /staff_overflow/sdavid-tmp/dec04/swope235/pep/aay01556.geneseqp1990a
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8: /staff_overflow/sdavid-tmp/dec04/swope235/pep/us-08-128-299-1.*
9: /staff_overflow/sdavid-tmp/dec04/swope235/pep/atrp.streq.uniprot.spd
10: /staff_overflow/sdavid-tmp/dec04/swope235/pep/us-09-211-542a-6.*
11: /staff_overflow/sdavid-tmp/dec04/swope235/pep/us-08-560-098a-52.*
12: /staff_overflow/sdavid-tmp/dec04/swope235/pep/us-09-211-542a-2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33.5	5.6	414	1	AAR10194
2	33.5	5.6	414	2	AAR63120
3	33.5	5.6	414	3	AAW94664
4	33.5	5.6	414	4	AAV01556
5	33.5	5.6	414	5	AAV24794
6	33.5	5.6	414	7	pct-us93-09502-1
7	33.5	5.6	414	8	us-08-128-299-1
8	33.5	5.6	414	10	us-09-211-542a-6
9	33.5	5.6	440	9	STREP STREQ
10	33.5	5.6	440	11	us-08-560-098a-52
11	33.5	5.6	795	6	AAV24797
12	33.5	5.6	795	12	us-09-211-542a-2

ALIGNMENTS

RESULT 1
AAR10194
ID AAR10194 standard; protein; 414 AA.
XX

AC AAR10194;
DT 28-MAR-1991 (first entry)
XX
DE Streptokinase encoded by synthetic gene.
XX
KW streptokinase; thrombolytic agent; myocardial infarction.
XX
OS Synthetic.
XX
PN EP407942-A.
XX
PD 16-JAN-1991.
XX
PF 11-JUL-1989; 89JP-00179432.
XX
PR 11-JUL-1989; 89JP-00179432.
XX
PR 27-NOV-1989; 89JP-00307957.
XX
PR 11-APR-1990; 90JP-00096830.
XX
PA (SAKA) OTSUKA PHARM FACTOR.
XX
PI Majima E, Ogino K, Ono K, Sakata Y, Uenoyama T;
XX
DR WPI; 1991-016179/03.
XX
DR N-PSDB; AAQ10230.
XX
PT Synthetic gene encoding streptokinase - scale, high purity prodn. of streptokinase used as a thrombolytic agent.
XX
PS Claim 1; Page 51; 76pp; English.
XX
CC Streptokinase and its derivatives can be produced in large quantities with high purity for use as thrombolytic agents in patients with lung CC thrombus or myocardial infarction. See also AAR10195-R10200
XX
SQ Sequence 414 AA;
Query Match 5.6%; Score 33.5; DB 1; Length 414;
Best Local Similarity 29.4%; Pred. No. 0;
Matches 10; Conservative 3; Mismatches 8; Indels 13; Gaps 2;
Oy 44 VCTCYGSGRGFNCESKPEAETCF-----DKYT 71
Db 364 IITVYMKR-----PEGENASVHLAYDKDRYT 390
RESULT 2
AAR63120
ID AAR63120 standard; protein; 414 AA.
XX
AC AAR63120;
XX
DT 16-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 16-NOV-1994 (first entry)
XX
DE Streptokinase.
XX
KW Streptokinase; SK; Streptococcus equisimilis; plasminogen;
XX
KW myocardial infarction.
XX
OS Streptococcus dysgalactiae subsp. equisimilis.
XX
FH Key Location/Qualifiers
FT Region 1..352
FT /note= "claim 3, see CC"
FT Region 14..414
FT /note= "claim 1, see CC"
FT Region 120..352
FT /note= "claim 3, see CC"
FT Region 244..414
FT /note= "claim 3, see CC"

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FT Region      244. .352
XX /note= "claim 2, see CC"
PN WO9407992-A1.
XX
XX 14-APR-1994.
PD
XX 05-OCT-1993; 93WO-US009502.
XX
XX 05-OCT-1992; 92US-00956692.
PR
XX 29-SEP-1993; 93US-00128299.
PR
XX
XX (GEO ) GEN HOSPITAL CORP.
PA
XX (HARD ) HARVARD COLLEGE.
PA
PI Reed GL;
XX
XX WPI; 1994-135561/16.
DR
XX
XX DNA encoding a polypeptide which binds to plasminogen and corresponds to
PT region of streptokinase - useful to detect plasminogen in a sample and to
PT treat myocardial infarction.
XX
XX Disclosure; Page 40-41; 62pp; English.
XX
XX Nucleic acid comprising a sequence encoding amino acids 14-414 of
CC streptokinase, which binds to plasminogen and does not have a sequence
CC comprising amino acids 60-414 is new. The polypeptide pref. comprises
CC amino acids 244-352, 1-352, 120-352 or 244-414. (Updated on 25-MAR-2003
CC to correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)
XX
XX Sequence 414 AA;
SQ
Query Match      5.6%; Score 33.5; DB 2; Length 414;
Best Local Similarity 29.4%; Pred. No. 0;
Matches 10; Conservative 3; Mismatches 8; Indels 13; Gaps 2;

QY 44 VCTCYGSGRGNCESKPEAETCF-----DKYT 71
Db 364 IITVYMKR-----PEGENASYHLAYDKDRYT 390

RESULT 3
AAW94664
ID AAW94664 standard; protein; 414 AA.
XX
XX AAW94664;
AC
XX
XX 17-OCT-2003 (revised)
DT 04-MAY-1999 (first entry)
XX
XX Streptococcus equisimilis native streptokinase.
DE
XX Streptococcus equisimilis H46A; streptokinase; mutant; fibrinolytic;
KW plasma clot; hydrolysis; haemolytic Streptococcus; plasminogen; plasmin;
KW serine protease; fibrin; blood clot; thrombolytic;
KW vascular thromboembolytic symptom; acute myocardial infarction;
KW fibrinolysis; resistance.
XX
XX Streptococcus dysgalactiae subsp. equisimilis.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 14
FT /note= "encoded by ACC"
XX
XX US5876999-A.
PN
XX
XX 02-MAR-1999.
PD
XX
XX 06-DEC-1995; 95US-00568393.
PF
XX
XX 06-DEC-1995; 95US-00568393.
PR
XX
XX

PA (NASC-) NAT SCI COUNCIL.
XX
XX Wu H;
PI
XX
XX WPI; 1999-189643/16.
DR
XX N-PSDB; AAX16632.
DR
XX
XX Mutant streptokinase polypeptide - useful as plasmin-resistant
PT thrombolytic agent.
XX
XX Claim 1; Col 7-10; 17pp; English.
PS
XX
XX The present invention describes a mutant streptokinase (SK) polypeptide
CC in which at least one of the amino acids in the Pro8-Lys59-Ser60-Lys61
CC segment of the corresponding native SK is replaced by another amino acid.
CC The present sequence represents native SK. SK is a secretory protein of
CC haemolytic Streptococcus able to activate human plasminogen (HPIg) to
CC plasmin (HPIm), which is a serine protease able to catalyse the
CC hydrolysis of fibrin in blood clots. The SK is useful as a thrombolytic
CC agent in the treatment of vascular thromboembolytic symptoms such as
CC acute myocardial infarction. Compared with wild-type SK, the K59E mutant
CC is more resistant to degradation by human plasmin and is more effective
CC both in acting as a fibrinolytic agent and in activating human plasminogen.
CC (Updated on 17-OCT-2003 to standardise OS field)
XX
XX Sequence 414 AA;
SQ
Query Match      5.6%; Score 33.5; DB 3; Length 414;
Best Local Similarity 29.4%; Pred. No. 0;
Matches 10; Conservative 3; Mismatches 8; Indels 13; Gaps 2;

QY 44 VCTCYGSGRGNCESKPEAETCF-----DKYT 71
Db 364 IITVYMKR-----PEGENASYHLAYDKDRYT 390

RESULT 4
AAY01556
ID AAY01556 standard; peptide; 414 AA.
XX
XX AAY01556;
AC
XX
XX 17-OCT-2003 (revised)
DT 18-JUN-1999 (first entry)
XX
XX Native streptokinase protein sequence.
DE
XX Antigenic peptide; streptokinase; streptokinase-specific antibody;
KW thrombolytic activity; thrombolytic therapy; glomerulonephritis;
KW rheumatic fever.
XX
XX Streptococcus dysgalactiae subsp. equisimilis.
OS
XX
XX WO9908698-A1.
PN
XX
XX 25-FEB-1999.
PD
XX
XX 18-AUG-1998; 98WO-US017114.
PF
XX
XX 18-AUG-1997; 97US-0055911P.
PR
XX
XX (HARD ) HARVARD COLLEGE.
PA (GEO ) GEN HOSPITAL CORP.
XX
XX Reed GL, Parhami-Seren B;
PI
XX WPI; 1999-190113/16.
DR
XX
XX New polypeptides which bind streptokinase-specific antibodies - useful in
PT thrombolytic therapy.
XX
XX Disclosure; Page 12; 44pp; English.
XX

```

```

CC presence of fibrin than in the absence of fibrin. The modified
CC streptokinase has at least one amino acid substitution that inactivates a
CC substrate site for proteolytic cleavage. This reduces the rate of
CC degradation of the streptokinase at least two-fold. The present sequence
CC represents native streptokinase (nsk). (Updated on 17-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 414 AA;

Query Match 5.6%; Score 33.5; DB 5; Length 414;
Best Local Similarity 29.4%; Pred. No. 0;
Matches 10; Conservative 3; Mismatches 8; Indels 13; Gaps 2;

QY 44 VTCYGGSRGFNCESKPEAEETCF-----DKYT 71
: ||| ||| ||| : |||
Db 364 IITVYMGKR-----PEGENASYHLAYDKDRYT 390

RESULT 6
pct-us93-09502-1

Query Match 5.6%; Score 33.5; DB 7; Length 414;
Best Local Similarity 29.4%; Pred. No. 0;
Matches 10; Conservative 3; Mismatches 8; Indels 13; Gaps 2;

QY 44 VTCYGGSRGFNCESKPEAEETCF-----DKYT 71
: ||| ||| ||| : |||
Db 364 IITVYMGKR-----PEGENASYHLAYDKDRYT 390

RESULT 7
us-08-128-299-1

Query Match 5.6%; Score 33.5; DB 8; Length 414;
Best Local Similarity 29.4%; Pred. No. 0;
Matches 10; Conservative 3; Mismatches 8; Indels 13; Gaps 2;

QY 44 VTCYGGSRGFNCESKPEAEETCF-----DKYT 71
: ||| ||| ||| : |||
Db 364 IITVYMGKR-----PEGENASYHLAYDKDRYT 390

RESULT 8
us-09-211-542a-6

Query Match 5.6%; Score 33.5; DB 10; Length 414;
Best Local Similarity 29.4%; Pred. No. 0;
Matches 10; Conservative 3; Mismatches 8; Indels 13; Gaps 2;

QY 44 VTCYGGSRGFNCESKPEAEETCF-----DKYT 71
: ||| ||| ||| : |||
Db 364 IITVYMGKR-----PEGENASYHLAYDKDRYT 390

RESULT 9
STRP_STRP
ID_STRP_STRP STANDARD; PRT; 440 AA.
AC P00779;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Streptokinase C precursor.
GN Name=ekc;
OS Streptococcus equisimilis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=119602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H46A;
RX MSDLINE=85232082; PubMed=2989113;
RA Malke H., Roe B., Ferretti J.J.;
RT "Nucleotide sequence of the streptokinase gene from Streptococcus

```

```
RT equisimilis H46A." ;
RL Gene 34:357-362 (1985).
RN [2]
RP SEQUENCE OF 27-440.
RX MEDLINE=83127125; PubMed=6760891;
RA Jackson K.W., Tang J.;
RT "Complete amino acid sequence of streptokinase and its homology with
RL Biochemistry 21:6620-6625 (1982).
CC !- FUNCTION: This protein is not a protease, but it activates
CC plasminogen by complexing with it. As a potential virulence
CC factor, it is thought to prevent the formation of effective fibrin
CC barriers around the site of infection, thereby contributing to the
CC invasiveness of the cells.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K02986; AAA26974.1; -.
DR EMBL; X72832; CAA51351.1; -.
DR PIR; A00967; BZSO.
DR PIR; A22801; A22801.
DR PDB; 1L4D; X-ray; B=40-173.
DR PDB; 1L4Z; X-ray; B=26-173.
DR PDB; 1QOR; X-ray; A/B/C/D=177-314.
DR InterPro; IPR004093; Streptokinase.
DR InterPro; IPR008124; Streptokinase.
DR Pfam; PF02821; Staphylokinase; 3.
DR PRINTS; PR01753; STREPKINASE.
KW 3D-structure; Direct protein sequencing; Plasminogen activation;
KW Signal; Virulence.
FT SIGNAL 1 26
FT CHAIN 27 440 Streptokinase C.
FT VARIANT 195 195 L -> D.
FT VARIANT 207 207 D -> L.
FT CONFLICT 298 300 EKY -> LEYK (in Ref. 2).
FT CONFLICT 438 438 N -> D (in Ref. 2).
FT STRAND 180 180
FT STRAND 184 194
FT TURN 199 200
FT TURN 203 204
FT STRAND 205 205
FT STRAND 209 214
FT TURN 216 217
FT STRAND 219 221
FT HELIX 222 236
FT TURN 238 239
FT STRAND 240 252
FT TURN 253 254
FT STRAND 259 260
FT STRAND 268 270
FT STRAND 275 275
FT STRAND 278 280
FT TURN 282 284
FT STRAND 287 289
FT STRAND 292 304
FT TURN 305 306
FT SEQUENCE 440 AA; 50140 MW; 8FC1F22648ACC77A CRC64;

Query Match 5.6%; Score 33.5; DB 9; Length 440;
Best Local Similarity 29.4%; Pred. No. 0;
Matches 10; Conservative 3; Mismatches 8; Indels 13; Gaps 2;

QY 44 VCTCYGSGRGNCESKPEAEETCF-----DKYT 71
: ||| ||| :
DB 390 IITVYMKR-----PEGENASYHLAYDKDRYT 416

RESULT 10
us-08-560-098a-52
Query Match 5.6%; Score 33.5; DB 11; Length 440;
Best Local Similarity 29.4%; Pred. No. 0;
Matches 10; Conservative 3; Mismatches 8; Indels 13; Gaps 2;

QY 44 VCTCYGSGRGNCESKPEAEETCF-----DKYT 71
: ||| ||| :
DB 390 IITVYMKR-----PEGENASYHLAYDKDRYT 416

RESULT 11
AAAY24797
ID AAY24797 standard; protein; 795 AA.
XX
AC AAY24797;
XX
DT 26-AUG-1999 (first entry)
XX
DE Streptokinase and maltose binding protein fusion protein.
XX
KW Streptococcus; streptokinase; fibrin-dependent plasminogen activator;
KW nSK; rSK; bacterial; blood clot; thrombotic condition;
KW myocardial infarction; venous thrombosis; pulmonary embolism;
KW cerebral thrombosis; graft thrombosis; arterial thrombosis.
XX
OS Streptococcus dysgalactiae subsp. equisimilis.
OS Synthetic.
XX
XX WO9931247-A1.
XX
XX 24-JUN-1999.
XX
XX 15-DEC-1998; 98WO-US026694.
XX
XX 15-DEC-1997; 97US-0069497P.
XX (HARD ) HARVARD COLLEGE.
XX
XX Reed GL;
XX
XX WPI; 1999-395183/33.
XX
XX N-PSDB; AAX80497.
XX
XX N-terminally deleted streptokinase.
XX
XX Example; Page 48-51; 73pp; English.
XX
XX The present invention describes an isolated bacterial protein that
XX induces fibrin-dependent plasminogen activation in a pharmaceutical
XX composition for dissolving blood clots. Also described are: (1) a
XX composition comprising an isolated modified streptokinase, the
XX modification comprising removal of amino acid residues in the amino terminus;
XX (2) a method for dissolving a blood clot in a subject, comprising
XX administering to the subject a fibrin-dependent streptokinase protein; a
XX nucleic acid (1) encoding a modified bacterial streptokinase; (3) an
XX expression vector comprising (1); and (4) a host cell transformed with
XX the expression vector of (3). The pharmaceutical composition comprising a
XX bacterial fibrin-dependent plasminogen activator is useful for dissolving
XX blood clots in patients with a thrombotic condition, e.g. myocardial
XX infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis,
XX graft thrombosis and arterial thrombosis. The modified streptokinase can
XX also be used in non-human mammals. Streptokinase activation of
XX plasminogen is at least 10-fold, preferably 100-fold greater in the
XX presence of fibrin than in the absence of fibrin. The modified
XX streptokinase has at least one amino acid substitution that inactivates a
XX substrate site for proteolytic cleavage. This reduces the rate of
XX degradation of the streptokinase at least two-fold. The present sequence
XX represents a streptokinase and maltose binding protein fusion protein
XX from an example of the present invention
XX
XX Sequence 795 AA;
```


Query Match 5.6%; Score 33.5; DB 6; Length 795;
Best Local Similarity 29.4%; Pred. No. 0;
Matches 10; Conservative 3; Mismatches 8; Indels 13; Gaps 2;
QY 44 VCTCYGSRGFNCESKPEAEETCF-----DKYT 71
DB 745 IITVYMGKR-----PEGENASYHLAYDKDRYT 771

RESULT 12
us-09-211-542a-2

Query Match 5.6%; Score 33.5; DB 12; Length 795;
Best Local Similarity 29.4%; Pred. No. 0;
Matches 10; Conservative 3; Mismatches 8; Indels 13; Gaps 2;
QY 44 VCTCYGSRGFNCESKPEAEETCF-----DKYT 71
DB 745 IITVYMGKR-----PEGENASYHLAYDKDRYT 771

Search completed: December 6, 2004, 14:53:45
Job time : 1 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 6, 2004, 15:02:16 ; Search time 2 Seconds
(without alignments)
2.629 Million cell updates/sec

Title: US-09-940-235-4
Perfect score: 627
Sequence: 1 PIAKCFDHAAGTSYVVGST.....ERHTSVQTTSGSGPFTDVR 110

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 10 seqs, 23900 residues

Total number of hits satisfying chosen parameters: 20

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 20 summaries

Command line parameters:
-MODEL=frame_p2n.model
-DB=-SUFFIX=ptc -OUT=align4_150_259_seq -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=150 -END=259 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=20
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=20 -MODE=LOCAL
-OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -NCPU=6
-NO_XLPXY -NEG SCORES=0 -LONGLOG -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
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2: /staff_overflow/sdavid-tmp/dec04/swope235/seq/e03308.gb.pat.*
3: /staff_overflow/sdavid-tmp/dec04/swope235/seq/105204.gb.pat.*
4: /staff_overflow/sdavid-tmp/dec04/swope235/seq/sedexb.gb.pat.*
5: /staff_overflow/sdavid-tmp/dec04/swope235/seq/atrksc.gb.pat.*
6: /staff_overflow/sdavid-tmp/dec04/swope235/seq/aa16632.Geneseqm19908
7: /staff_overflow/sdavid-tmp/dec04/swope235/seq/aa80497.Geneseqm19908
8: /staff_overflow/sdavid-tmp/dec04/swope235/seq/aa80497.Geneseqm19908
9: /staff_overflow/sdavid-tmp/dec04/swope235/seq/us-09-211-542a-5.*
10: /staff_overflow/sdavid-tmp/dec04/swope235/seq/us-08-568-393b-1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	41	6.5	8931	4 SEDXB	ACCESSION:X72832
2	39	6.2	8931	4 SEDXB	ACCESSION:X72832
C 3	33.5	5.3	1242	6 AAX16632	Streptococcus equi
C 4	33.5	5.3	1242	7 AAX80492	Streptococcus equi
C 5	33.5	5.3	1242	9 us-09-211-542a-5	
C 6	33.5	5.3	1242	10 us-08-568-393b-1	
C 7	33.5	5.3	1401	3 I05204	ACCESSION:I05204
C 8	33.5	5.3	2385	1 AR143998	ACCESSION:AR143998
C 9	33.5	5.3	2385	8 AAX80497	Streptokinase and
C 10	33.5	5.3	2568	5 STRSKC	ACCESSION:K02986
11	33	5.3	2385	1 AR143998	ACCESSION:AR143998

12 33 5.3 2385 8 AAX80497 Streptokinase and
13 31.5 5.0 1242 6 AAX16632 Streptococcus equi
14 31.5 5.0 1242 7 AAX80492 Streptococcus equi
15 31.5 5.0 1242 9 us-09-211-542a-5
16 31.5 5.0 1242 10 us-08-568-393b-1
17 31.5 5.0 1242 2 E03308 ACCESSION:E03308
18 31.5 5.0 1401 3 I05204 ACCESSION:I05204
19 31.5 5.0 2568 5 STRSKC ACCESSION:K02986
c 20 27 4.3 1262 2 E03308 ACCESSION:E03308

ALIGNMENTS

RESULT 1
SEDEXB/c
LOCUS SEDXB 8931 bp DNA linear BCT 17-FEB-1997
DEFINITION S equisimilis dexb, abc, lrp, skc, rel genes and ORF1.
ACCESSION X72832
VERSION X72832.1 GI:407876
KEYWORDS abc gene; ABC transporter; dexB gene; dextran glucosidase; glucan 1,6-alpha-glucosidase; leucine rich protein; LRP gene; ORF1; rel gene; skc gene; streptokinase; stringent response-like protein.
SOURCE Streptococcus dysgalactiae subsp. equisimilis
ORGANISM Streptococcus dysgalactiae subsp. equisimilis
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
REFERENCE 1 (bases 3621 to 6190)
AUTHORS Malke,H., Roe,B. and Ferretti,J.J.
TITLE Nucleotide sequence of the streptokinase gene from Streptococcus equisimilis H46A
JOURNAL Gene 34 (2-3), 357-362 (1985)
MEDLINE 85232082
PUBMED 2989113
REFERENCE 2 (bases 1 to 4188; 5790 to 8931)
AUTHORS Mechold,U., Steiner,K., Vettermann,S. and Malke,H.
TITLE Genetic organization of the streptokinase region of the Streptococcus equisimilis H46A chromosome
JOURNAL Mol. Gen. Genet. 241 (1-2), 129-140 (1993)
MEDLINE 94049672
PUBMED 8232196
REFERENCE 3 (bases 1 to 8931)
AUTHORS Malke,H.
TITLE Direct Submission
COMMENT Submitted (05-MAY-1993) H. Malke, Institute for Molecular Biology, Jena University, Winzerlaer Str 10, 07708 Jena, FRG
Related sequences: K02986, M19346, X13399 & X13400.
FEATURES
Location/Qualifiers
source 1. .8931
/organism="Streptococcus dysgalactiae subsp. equisimilis"
/mol_type="genomic DNA"
/strain="H46A"
/isolate="human group C strain"
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/db_xref="taxon:119602"
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KQDLNWEAHVROKIYDMNFWIAKGIIGFGRMDVIDLGKI PDSEITGNPRLHDYL
KEMNOATFGNHDVMTGETWGATPEIARQYSRPENKELSMVFOFHVGLQHKPNAPKW
DYAELDVPALKTIIFSQWTELKLGEGWNSLFWNHDLPRVLISWGNDSIYRKSKAKA
LAILHLMRGTPIYQGBEIGMTNYPFKDLTEVDDIESLNYAKEMENGVPFAARVSS
IRKVGDNARTPMQSKDTHAGSEAOETWLPVNPYQEIINVADALANODSIPTTYQQ
LIALRKQDWLVEADYVHLLPTADKVFAYQORQGEETVIYVNVSDQEQVPAKDLAGE
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complement(2644)
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/genes="abc"
/notes="(+) frame shift mutation in H46A"
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/notes="Walker motif A"
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QIAGLEVLIPTSTQTLFRCQATSIKVLRSLEGLPTLESDFGLALTFMFGNAWYQ
VAAIGLRCEFECCQLLTAYLKQKSGGLITFAEVLWSILSHQSPALTRQPHQFIN
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Alignment Scores:
Pred. No.:
Score:

1.62
41.00
Length:
Matches:
8931
11

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ADLLKAIQLIANVHNSDDYFVIDFASDATITDRNGKYVFADKGSVTLPTQPVQE
FLLSGHVRVPYKEPIQOAKSDVVEYTVQTFPLNPDGDFRPLGKDTKLLKTALIGD
TITSOELLAQAQSIILNKHGTYIYERDSSIIVHDNDIPRTILPMDQEFYRVKNREQ
AYRINKSGNEINNTDLISEKYVYLKKEKYPDPDRSHLKLFTIKYVDVDTNELL
KSEQLTASERNLDFRDLDIPDKAKLITNNLDAFGIMDTILFGKVEDNDDTNRIT
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CC agent in the treatment of vascular thromboembolytic symptoms such as
 CC acute myocardial infarction. Compared with wild-type SK, the K59E mutant
 CC is more resistant to degradation by human plasmin and is more effective
 CC both in acting as a fibrolytic agent and in activating human plasminogen.
 CC (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 1242 BP; 423 A; 268 C; 237 G; 314 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2.19 Length: 1242
 Score: 33.50 Matches: 10
 Percent Similarity: 41.94% Conservatives: 3
 Best Local Similarity: 32.26% Mismatches: 6
 Query Match: 5.34% Indels: 12
 DB: Gaps: 1

US-09-940-235-4 (1-259) x AAX16632 (1-1242)

Qy 168 GluThrTrpGlu-LysProTyrGlnGlyTrpMetMetValaspCysThr----- 183
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 Db 537 GAGACCTGGTCTGAAATCGTCATCAGGGTTTAAAGGGAGTAAACTGTACAGTATATTCAC 478
 |||||

Qy 184 -----CysLeuGly 186
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Db 477 ATCAACAGATTTCGCTTGGTTTGTATGGT 447

RESULT 4

ID AAX80492/c
 XX AAX80492 standard; cDNA; 1242 BP.
 AC AAX80492;
 XX
 XX 17-OCT-2003 (revised)
 DT 26-AUG-1999 (first entry)
 XX
 XX Streptococcus equisimilis native streptokinase encoding cDNA.
 DE
 XX
 KW Streptococcus; streptokinase; fibrin-dependent plasminogen activator;
 KW nSK; rSK; bacterial; blood clot; thrombotic condition;
 KW myocardial infarction; venous thrombosis; pulmonary embolism;
 KW cerebral thrombosis; graft thrombosis; arterial thrombosis; ss.
 XX
 OS Streptococcus dysgalactiae subsp. equisimilis.
 XX
 PN WO931247-A1.
 XX
 XX 24-JUN-1999.
 PD
 XX
 XX 15-DEC-1998; 98WO-US026694.
 PF
 XX
 XX 15-DEC-1997; 97US-0069497P.
 PR
 XX
 XX (HARD) HARVARD COLLEGE.
 PA
 XX
 XX Reed GL;
 PI
 XX
 XX WPI: 1999-395183/33.
 DR
 XX
 XX P-PSDB; AAY24794.
 DR
 XX
 XX N-terminally deleted streptokinase.
 PT
 XX
 XX Claim 44; Page 58-60; 73pp; English.
 PS
 XX
 XX The present invention describes an isolated bacterial protein that
 CC induces fibrin-dependent plasminogen activation in a pharmaceutical
 CC composition for dissolving blood clots. Also described are: (1) a
 CC composition comprising an isolated modified streptokinase, the
 CC modification being removal of amino acid residues in the amino terminus;
 CC (2) a method for dissolving a blood clot in a subject, comprising
 CC administering to the subject a fibrin-dependent streptokinase protein; a
 CC nucleic acid (1) encoding a modified bacterial streptokinase; (3) an
 CC expression vector comprising (1); and (4) a host cell transformed with
 CC the expression vector of (3). The pharmaceutical composition comprising a

CC bacterial fibrin-dependent plasminogen activator is useful for dissolving
 CC blood clots in patients with a thrombotic condition, e.g. myocardial
 CC infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis,
 CC graft thrombosis and arterial thrombosis. The modified streptokinase can
 CC also be used in non-human mammals. Streptokinase activation of
 CC plasminogen is at least 10-fold, preferably 100-fold greater in the
 CC presence of fibrin than in the absence of fibrin. The modified
 CC streptokinase has at least one amino acid substitution that inactivates a
 CC substrate site for proteolytic cleavage. This reduces the rate of
 CC degradation of the streptokinase at least two-fold. The present sequence
 CC encodes native streptokinase (nSK). (Updated on 17-OCT-2003 to
 CC standardise OS field)

XX Sequence 1242 BP; 424 A; 267 C; 237 G; 314 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2.19 Length: 1242
 Score: 33.50 Matches: 10
 Percent Similarity: 41.94% Conservatives: 3
 Best Local Similarity: 32.26% Mismatches: 6
 Query Match: 5.34% Indels: 12
 DB: Gaps: 1

US-09-940-235-4 (1-259) x AAX80492 (1-1242)

Qy 168 GluThrTrpGlu-LysProTyrGlnGlyTrpMetMetValaspCysThr----- 183
 |||||
 Db 537 GAGACCTGGTCTGAAATCGTCATCAGGGTTTAAAGGGAGTAAACTGTACAGTATATTCAC 478
 |||||

Qy 184 -----CysLeuGly 186
 |||||

Db 477 ATCAACAGATTTCGCTTGGTTTGTATGGT 447

RESULT 5

us-09-211-542a-5/c

Alignment Scores:
 Pred. No.: 2.19 Length: 1242
 Score: 33.50 Matches: 10
 Percent Similarity: 41.94% Conservatives: 3
 Best Local Similarity: 32.26% Mismatches: 6
 Query Match: 5.34% Indels: 12
 DB: Gaps: 1

US-09-940-235-4 (1-259) x us-09-211-542a-5 (1-1242)

Qy 168 GluThrTrpGlu-LysProTyrGlnGlyTrpMetMetValaspCysThr----- 183
 |||||
 Db 537 GAGACCTGGTCTGAAATCGTCATCAGGGTTTAAAGGGAGTAAACTGTACAGTATATTCAC 478
 |||||

Qy 184 -----CysLeuGly 186
 |||||

Db 477 ATCAACAGATTTCGCTTGGTTTGTATGGT 447

RESULT 6

us-08-568-393b-1/c

Alignment Scores:
 Pred. No.: 2.19 Length: 1242
 Score: 33.50 Matches: 10
 Percent Similarity: 41.94% Conservatives: 3
 Best Local Similarity: 32.26% Mismatches: 6
 Query Match: 5.34% Indels: 12
 DB: Gaps: 1

US-09-940-235-4 (1-259) x us-08-568-393b-1 (1-1242)

Qy 168 GluThrTrpGlu-LysProTyrGlnGlyTrpMetMetValaspCysThr----- 183
 |||||
 Db 537 GAGACCTGGTCTGAAATCGTCATCAGGGTTTAAAGGGAGTAAACTGTACAGTATATTCAC 478
 |||||

Qy 184 -----CysLeuGly 186
 |||||

Db	1620 ATCAACAGATTTCGCTGGTTTGTATTGGT 1590	477 ATCAACAGATTTCGCTGGTTTGTATTGGT 447
Db	1620 ATCAACAGATTTCGCTGGTTTGTATTGGT 1590	477 ATCAACAGATTTCGCTGGTTTGTATTGGT 447
RESULT 7		
LOCUS	105204 1401 bp DNA linear PAT 02-DEC-1994	105204 1401 bp DNA linear PAT 02-DEC-1994
DEFINITION	Sequence 5 from Patent EP 0248227.	Sequence 5 from Patent EP 0248227.
ACCESSION	105204	105204
VERSION	105204.1	105204.1
KEYWORDS	GI:591209	GI:591209
SOURCE	Unknown.	Unknown.
ORGANISM	Unknown.	Unknown.
REFERENCE	Unclassified.	Unclassified.
AUTHORS	1 (bases 1 to 1401)	1 (bases 1 to 1401)
TITLE	Hagenson,M.J. and Stroman,D.W.	Hagenson,M.J. and Stroman,D.W.
JOURNAL	Yeast production of streptokinase	Yeast production of streptokinase
FEATURES	Patent: EP 0248227-A1 5 09-DEC-1987; Location/Qualifiers	Patent: EP 0248227-A1 5 09-DEC-1987; Location/Qualifiers
source	1..1401	1..1401
	/organism="unknown"	/organism="unknown"
	/mol_type="unassigned DNA"	/mol_type="unassigned DNA"
Alignment Scores:		
Pred. No.:	2.98	Length: 1401
Score:	33.50	Matches: 10
Percent Similarity:	41.94%	Conservative: 3
Best Local Similarity:	32.26%	Mismatches: 6
Query Match:	5.34%	Indels: 12
DB:	3	Gaps: 1
US-09-940-235-4 (1-259) x 105204 (1-1401)		
Qy	168 GluThrTrpGlu-LysProTyrGlnGlyTrpMetMetValAspCysThr----- 183	
Db	546 GAGACCTGGTCTGAATCGTCATCAGGGTTTAAGGAGTAACTGTACAGTATATCCAC 487	
Qy	184 -----CysLeuGly 186	
Db	486 ATCAACAGATTTCGCTGGTTTGTATTGGT 456	
RESULT 8		
LOCUS	AR143998 2385 bp DNA linear PAT 08-AUG-2001	AR143998 2385 bp DNA linear PAT 08-AUG-2001
DEFINITION	Sequence 1 from patent US 6210667.	Sequence 1 from patent US 6210667.
ACCESSION	AR143998	AR143998
VERSION	AR143998.1	AR143998.1
KEYWORDS	GI:15105865	GI:15105865
SOURCE	Unknown.	Unknown.
ORGANISM	Unknown.	Unknown.
REFERENCE	Unclassified.	Unclassified.
AUTHORS	1 (bases 1 to 2385)	1 (bases 1 to 2385)
TITLE	Bacterial fibrin-dependent plasminogen activator	Bacterial fibrin-dependent plasminogen activator
JOURNAL	Patent: US 6210667-A 1 03-APR-2001; Location/Qualifiers	Patent: US 6210667-A 1 03-APR-2001; Location/Qualifiers
FEATURES	1..2385	1..2385
source	/organism="unknown"	/organism="unknown"
	/mol_type="unassigned DNA"	/mol_type="unassigned DNA"
Alignment Scores:		
Pred. No.:	10	Length: 2385
Score:	33.50	Matches: 10
Percent Similarity:	41.94%	Conservative: 3
Best Local Similarity:	32.26%	Mismatches: 6
Query Match:	5.34%	Indels: 12
DB:	1	Gaps: 1
US-09-940-235-4 (1-259) x AR143998 (1-2385)		
Qy	168 GluThrTrpGlu-LysProTyrGlnGlyTrpMetMetValAspCysThr----- 183	
Db	1680 GAGACCTGGTCTGAATCGTCATCAGGGTTTAAGGAGTAACTGTACAGTATATCCAC 1621	
Qy	184 -----CysLeuGly 186	

```
US-09-940-235-4 (1-259) x AAX80497 (1-2385)

Qy 168 GluThrTrpGlu-LysProTyrGlnGlyTrpMetMetValaspCysThr----- 183
Db 1680 GAGACCTGGTCTGAATCGTCATCAGGGTTTAAGGGAGTAACACTGTACAGTATATCCAC 1374
Qy 184 -----CysLeuGly 186
Db 1620 ATCAACAGATTTCGCTGGTTTGTATTGGT 1590

RESULT 10
STRSKC/c
LOCUS STRSKC 2568 bp DNA linear BCT 26-APR-1993
DEFINITION Streptococcus equisimilis (H46A) streptokinase gene, complete cds.
ACCESSION K02986
VERSION K02986.1 GI:153808
KEYWORDS streptokinase.
SOURCE Streptococcus dysgalactiae subsp. equisimilis
ORGANISM Streptococcus dysgalactiae subsp. equisimilis
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
REFERENCE 1 (bases 1 to 2568)
AUTHORS Malke,H.; Roe,B. and Ferretti,J.J.
TITLE Nucleotide sequence of the streptokinase gene from Streptococcus
equisimilis H46A
JOURNAL Gene 34 (2-3), 357-362 (1985)
MEDLINE 85232082
PUBMED 2989113
COMMENT Original source text: S.equisimilis (strain H46A) DNA, clone pMF5.
Draft entry and hard copy of sequence for [1] kindly provided by
J.J.Ferretti, 03-SEP-1985.
The -35 and -10 regions are located at positions 760-765 and
781-786 respectively and an SD sequence at 808-813. Downstream
from the coding region inverted repeats (positions 2176-2190 and
2203-2217) are thought to function as transcription terminators.
The nucleotide sequence of skc does not support the hypothesis that
the gene has evolved by duplication and fusion, as suggested by
internal two-fold AA homologies of its product.
FEATURES
Location/Qualifiers
1..2568
/organism="Streptococcus dysgalactiae subsp. equisimilis"
/mol_type="genomic DNA"
/db_xref="taxon:119602"
794..>2141
/product="skc mRNA"
819..2141
/notes="prestreptokinase"
/codon_start=1
/transl_table=11
/protein_id="AA26974.1"
/db_xref="GI:153809"
/translation="MKNYLSFGFMALLFALTFTVNSVQIAIGPEWLLDRPSVNSQL
VVSVAGTVEGTNQDI SLKFEIDLTSPAHGGTEQGLSPKSPFATDSGAMSHKLEK
ADLLKAIQEOIANVNSDDYFEVIDFASDATITDRNGKVYFADKQDSVTLPTQPOVE
FLLSGHVRVPYKEKPIQONAKSVQVVEYTVQFTPLNPDDDFRPLKDTLLKLTLAGD
FTLSQLLAQASIKNRPYCYTIYERDSIVTHDNDIETIILPMQOEFTYRKNRQ
ATRKNGSLGNEINNDLISEKYVLLKNGKEGIDFDFRSHLKLFTIKYVDVDNELL
KESQLTAGERNLDFDLDPDRKAKLLYNLDAFGIMDYTLTGKVEDNHDHDTNRIIT
VYMGKPEGENASVHLAYDKRDTYEBEREVYSYLRVTGTPIPNPNDK"
sig_peptide 819..896
/notes="streptokinase signal peptide"
mat_peptide 897..2138
/product="streptokinase"

Alignment Scores:
Pred. No.: 11 5 Length: 2568
Score: 33.50 Matches: 10
Percent Similarity: 41.94% Conservative: 3
Best Local Similarity: 32.26% Mismatches: 6
Query Match: 5.34% Indels: 12
DB: 5 Gaps: 1

US-09-940-235-4 (1-259) x STRSKC (1-2568)

Qy 168 GluThrTrpGlu-LysProTyrGlnGlyTrpMetMetValaspCysThr----- 183
Db 1680 GAGACCTGGTCTGAATCGTCATCAGGGTTTAAGGGAGTAACACTGTACAGTATATCCAC 1374
Qy 184 -----CysLeuGly 186
Db 1620 ATCAACAGATTTCGCTGGTTTGTATTGGT 1590

RESULT 11
AR143998
LOCUS AR143998 2385 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6210667.
ACCESSION AR143998
VERSION AR143998.1 GI:15105865
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2385)
AUTHORS Reed,G.L.
TITLE Bacterial fibrin-dependent plasminogen activator
JOURNAL Patent: US 6210667-A 1 03-APR-2001;
FEATURES Location/Qualifiers
source 1..2385
/organism="unknown"
/mol_type="unassigned DNA"

Alignment Scores:
Pred. No.: 12 8 Length: 2385
Score: 33.00 Matches: 22
Percent Similarity: 30.19% Conservative: 10
Best Local Similarity: 20.75% Mismatches: 42
Query Match: 5.26% Indels: 32
DB: 1 Gaps: 5

US-09-940-235-4 (1-259) x AR143998 (1-2385)

Qy 151 IleAlaGluLysCysPheAspHisAlaAlaGlyThrSerTyrValValGlyGluThrTirp 170
Db 907 GTAGCGCTGAAGTCTTACGAGAGAGAGTTGGCGAAAGATCCAGTATTGCCGCCCATG 966
Qy 171 GluLysProTyrGlnGly-----TrpMet 178
Db 967 GAAACGCCAGAAAGGTGAAATCATCCGACATCCGAGATGTCGGTTCCTGGTAT 1026
Qy 179 MetValaspCysThrCysLeuGlyGluGlySerGlyArgIleThrCysThrSerArgasn 198
Db 1027 GCCGTGCGTACTGCGGTGATCAACGCCGCGCAGCGTCTGCAGACTGTCGAT-----GAA 1080
Qy 199 ArgCysasnaspGlnaspThrArgThrSerTyrargileGlyaspThrTrpSerLysLys 218
Db 1081 GCCCTGAAAGACGCCGAGACTAATTCGAGCTCGGTACCCGCG----- 1122
Qy 219 AspAsnArgGlyAsnLeuLeuGlnCysIleCysThrGlyAsnGlyArg-----Gly 235
Db 1123 -----CGGGATTCATC-----GAGGTAGGATTGTGGACCT 1155
Qy 236 GluTrpLysCysGluArg 241
Db 1156 GAGTGGCTGTAGACCGT 1173

RESULT 12
AAX80497
ID AAX80497 standard; cDNA; 2385 BP.
XX
AC AAX80497;
XX
DT 26-AUG-1999 (first entry)
XX
DB Streptokinase and maltose binding protein fusion protein encoding cDNA.
XX
XX Streptococcus; streptokinase; fibrin-dependent plasminogen activator;
```



```

KW nSK, rSK; bacterial; blood clot; thrombotic condition;
KW myocardial infarction; venous thrombosis; pulmonary embolism;
KW cerebral thrombosis; graft thrombosis; arterial thrombosis; ss.
XX
OS Streptococcus dysgalactiae subsp. equisimilis.
OS Synthetic.
PN WO9931247-A1.
XX
PD 24-JUN-1999.
XX
PF 15-DEC-1998; 98WO-US026694.
XX
PR 15-DEC-1997; 97US-0069497P.
XX
PA (HARD ) HARVARD COLLEGE.
XX
PI Reed GL;
XX
DR WPI; 1999-395183/33.
DR P-PSDB; AAY24797.
XX
PT N-terminally deleted streptokinase.
XX
PS Example; Page 45-48; 73pp; English.
XX
CC The present invention describes an isolated bacterial protein that
CC induces fibrin-dependent plasminogen activation in a pharmaceutical
CC composition for dissolving blood clots. Also described are: (1) a
CC composition comprising an isolated modified streptokinase, the
CC modification being removal of amino acid residues in the amino terminus;
CC (2) a method for dissolving a blood clot in a subject, comprising
CC administering to the subject a fibrin-dependent streptokinase protein; a
CC nucleic acid (1) encoding a modified bacterial streptokinase; (3) an
CC expression vector comprising (1); and (4) a host cell transformed with
CC the expression vector of (3). The pharmaceutical composition comprising a
CC bacterial fibrin-dependent plasminogen activator is useful for dissolving
CC blood clots in patients with a thrombotic condition, e.g. myocardial
CC infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis,
CC graft thrombosis and arterial thrombosis. The modified streptokinase can
CC also be used in non-human mammals. Streptokinase activation of
CC plasminogen is at least 10-fold, preferably 100-fold greater in the
CC presence of fibrin than in the absence of fibrin. The modified
CC streptokinase has at least one amino acid substitution that inactivates a
CC substrate site for proteolytic cleavage. This reduces the rate of
CC degradation of the streptokinase at least two-fold. The present sequence
CC encodes a streptokinase and maltose binding protein fusion protein from
CC an example of the present invention
XX
SQ Sequence 2385 BP; 745 A; 547 C; 549 G; 544 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 12.8 Length: 2385
Score: 33.00 Matches: 22
Percent Similarity: 30.19% Conservative: 10
Best Local Similarity: 20.75% Mismatches: 42
Query Match: 5.26% Indels: 32
DB: 8 Gaps: 5

US-09-940-235-4 (1-259) x AAX80497 (1-2385)
QY 151 IleAlaGluLysCysPheAspHisAlaAlaGlyThrSerTyrValValGlyGluThrTrp 170
Db 907 GTAGCCCTGAAGTCTTACGAGGAGAGTTCGCGAAGATCCAGTATTCGCCGCACCATG 966
QY 171 GluLysProTyrGlnGly-----TriMet 178
Db 967 GAAACGCCCAAGAGGTGAATCATCGCAACATCCGCGAGATGTCGGCTTTCTGGTAT 1026
QY 179 MetValAspCysThrCysLeuGlyGluGlySerGlyAlaThrCysThrSerArgAsn 198
Db 1027 GCGTGCGTACTCGGTGATCAACGCCCGCGGGTGTGTCAGACTGTGCAT-----GAA 1080

199 ArgCysAsnAspGlnAspThrArgThrSerTyrArgIleGlyAspThrTrpSerLysLys 218
1081 GCCCTGAAGACGCGCAGACTAATTCGAGCTCGGTACCCGCG-----1122
QY 219 AspAsnArgGlyAsnLeuLeuGlnCysIleCysThrGlyAsnGlyArg-----Gly 235
Db 1123 -----CGGGGATCCATC-----GAGGGTAGATTGCTGGACCT 1155
QY 236 GluTriPlysCysGluArg 241
Db 1156 GAGTGGCTGCTAGACCT 1173

RESULT 13
AAX16632
ID AAX16632 standard; DNA; 1242 BP.
XX
AC AAX16632;
XX
DT 17-OCT-2003 (revised)
DT 04-MAY-1999 (first entry)
XX
DE Streptococcus equisimilis native streptokinase encoding DNA.
XX
KW Streptococcus equisimilis H46A; streptokinase; mutant; fibrinolytic;
KW plasma clot; hydrolysis; haemolytic Streptococcus; plasminogen; plasmin;
KW serine protease; fibrin; blood clot; thrombolytic;
KW vascular thromboembolytic symptom; acute myocardial infarction;
KW fibrinolysis; resistance; ds.
XX
OS Streptococcus dysgalactiae subsp. equisimilis.
XX
FH Key Location/Qualifiers
FT CDS 1..1242
FT /tag= a
FT /transl_except= (pos:40..42,aa:Asn)
FT /note= "no stop codon given"
XX
PN US5876999-A.
XX
PD 02-MAR-1999.
XX
PF 06-DEC-1995; 95US-00568393.
XX
PR 06-DEC-1995; 95US-00568393.
XX
PA (NASC-) NAT SCI COUNCIL.
XX
PI Wu H;
XX
DR WPI; 1999-189643/16.
DR P-PSDB; AAW94664.
XX
PT Mutant streptokinase polypeptide - useful as plasmin-resistant
PT thrombolytic agent.
PS Claim 1; Col 7-10; 17pp; English.
XX
CC The present invention describes a mutant streptokinase (SK) polypeptide
CC in which at least one of the amino acids in the Pro58-Lys59-Ser60-Lys61
CC segment of the corresponding native SK is replaced by another amino acid.
CC The present sequence encodes native SK. SK is a secretory protein of
CC haemolytic Streptococcus able to activate human plasminogen (HPLg) to
CC plasmin (HPLm) which is a serine protease able to catalyse the
CC hydrolysis of fibrin in blood clots. The SK is useful as a thrombolytic
CC agent in the treatment of vascular thromboembolytic symptoms such as
CC acute myocardial infarction. Compared with wild-type SK, the K59E mutant
CC is more resistant to degradation by human plasmin and is more effective
CC both in acting as a fibrinolytic agent and in activating human plasminogen.
CC (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 1242 BP; 423 A; 268 C; 237 G; 314 T; 0 U; 0 Other;

Alignment Scores:

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[illegible]

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QY 221 ArgGlyAsnLeuLeu-----GlnCysIleCysThrGlyAsnGlyArgGlyGluTrp 237
Db 595 -----TTACTAGCTCAAGCACAAAGCATTTTAAACAAAACCAACCCAGGCTATACG 645
QY 238 LysCysGluArgHisThrSerValGlnThr 247
Db 646 ATTTATGAACGTCGACTCTCTCAATCGTCACT 675

RESULT 17
LOCUS E03308 1262 bp DNA linear PAT 29-SEP-1997
DEFINITION DNA encoding recombinant streptokinase.
ACCESSION E03308
VERSION E03308.1 GI:2171525
KEYWORDS JP 1992011892-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 1262)
AUTHORS Fujii,S., Katano,T., Majima,E., Ogino,K., Ono,K., Sakata,Y. and Uenoyama,T.
TITLE PROTEIN OF STREPTOKINASES, CORRESPONDING GENE, CORRESPONDING PLASMID RECOMBINANT, CORRESPONDING CHARACTER TRANSFORMANT AND PRODUCTION
JOURNAL OTSUKA PHARMACEUTICAL FACTORY INC
COMMENT OS Artificial gene
PN JP 1992011892-A/1
PD 16-JAN-1992
PF 06-JUL-1990 JP 1990179851
PR 11-JUL-1989 JP 89P 179432, 27-NOV-1989 JP 89P 307957, PR 11-APR-1990 JP 90P 96830
PI FUJII SEISUO, KATANO TAMITAKA, MAJIMA EIJI, OGINO KOICHI, PI ONO KENJI,
PI SAKATA YASUYO, UENOYAMA TSUTOMU
PC C12N15/58, C12N1/21, C12N9/70, (C12N1/21, C12R1:19), (C12N9/70, PC C12R1:19);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: clone=pSKX;
FH Key Location/Qualifiers
FT 5'UTR 1..11
FT CDS 12..1256
FT /product='recombinant streptokinase' FT
mat_peptide 12..1253
FT /product='recombinant streptokinase' FT
3'UTR 1257..1263.
FEATURES
source
1..1262
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Alignment Scores:
Pred. No.: 8.58 Length: 1262
Score: 31.50 Matches: 16
Percent Similarity: 48.00% Conservative: 8
Best Local Similarity: 32.00% Mismatches: 17
Query Match: 5.02% Indels: 9
DB: 2 Gaps: 3

US-09-940-235-4 (1-259) x E03308 (1-1262)

QY 203 GlnAspThrArg-----ThrSerTyrArgIleGlyAspThrTrpSerLysLysAspAsn 220
Db 552 AAAGACACATAAAGTCGTGAAAACCCCTGGTCAACCATCATCTCTCAGGAG--- 608
QY 221 ArgGlyAsnLeuLeu-----GlnCysIleCysThrGlyAsnGlyArgGlyGluTrp 237

RESULT 18
LOCUS I05204 1401 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 5 from Patent EP 0248227.
ACCESSION I05204
VERSION I05204.1 GI:591209
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1401)
AUTHORS Hagenston,M.J. and Stroman,D.W.
TITLE Yeast production of streptokinase
JOURNAL Patent: EP 0248227-A1 5 09-DEC-1987;
FEATURES
source
1..1401
/organism='unknown'
/mol_type='unassigned DNA'

Alignment Scores:
Pred. No.: 10.5 Length: 1401
Score: 31.50 Matches: 16
Percent Similarity: 48.00% Conservative: 8
Best Local Similarity: 32.00% Mismatches: 17
Query Match: 5.02% Indels: 9
DB: 3 Gaps: 3

US-09-940-235-4 (1-259) x I05204 (1-1401)

QY 203 GlnAspThrArg-----ThrSerTyrArgIleGlyAspThrTrpSerLysLysAspAsn 220
Db 547 AAAGATACTAAGCTATTGAAAACACACTAGCTATCGGTGACACCATCATCTCAAGAA--- 603
QY 221 ArgGlyAsnLeuLeu-----GlnCysIleCysThrGlyAsnGlyArgGlyGluTrp 237
Db 604 -----TTACTAGCTCAAGCACAAAGCATTTTAAACAAAACCAACCCAGGCTATACG 654
QY 238 LysCysGluArgHisThrSerValGlnThr 247
Db 655 ATTTATGAACGTCGACTCTCTCAATCGTCACT 684

RESULT 19
LOCUS STRSKC 2568 bp DNA linear BCT 26-APR-1993
DEFINITION Streptococcus equisimilis (H46A) streptokinase gene, complete cds.
ACCESSION K02986
VERSION K02986.1 GI:153808
KEYWORDS streptokinase.
SOURCE Streptococcus dysgalactiae subsp. equisimilis
ORGANISM Streptococcus dysgalactiae subsp. equisimilis
REFERENCE 1 (bases 1 to 2568)
AUTHORS Malke,H., Roe,B. and Ferretti,J.J.
TITLE Nucleotide sequence of the streptokinase gene from Streptococcus equisimilis H46A
JOURNAL Gene 34 (2-3), 357-362 (1985)
MEDLINE 85232082
PUBMED 2989113
COMMENT Original source text: S.equisimilis (strain H46A) DNA, clone pMF5. Draft entry and hard copy of sequence for [1] kindly provided by J.J.Ferretti, 03-SEP-1985.
The -35 and -10 regions are located at positions 760-765 and 781-786 respectively and an SD sequence at 808-813. Downstream from the coding region inverted repeats (positions 2176-2190 and 2203-2217) are thought to function as transcription terminators.

```

The nucleotide sequence of skc does not support the hypothesis that the gene has evolved by duplication and fusion, as suggested by internal two-fold AA homologies of its product.

FEATURES

source	Location/Qualifiers
mRNA	1..2568 /organism="Streptococcus dysgalactiae subsp. equisimilis" /mol_type="genomic DNA" /db_xref="taxon:119602" 794..>2141 /product="skc mRNA"
CDS	819..2141 /note="prestreptokinase" /codon_start=1 /transl_table=11 /protein_id="AAA26974.1" /db_xref="GI:153809" /translation="MKNYLSFGFMALLFALTFGTVNSVQAIAGPEWLLDRPSSVNNSL VSVAGVTEGTNDIISLKPFEDILTSPAHGKTEQGLSPKSPFATDSCAMSHKLEK ADLLKAOEOLIANVNSNDYFEVIDFASDATIDRNGKUYFADKQGSVLTLPQVQAE FLSGHVVRPYKEKIQNQAQSVDEYTVQTFPLNPDDEFRLGDKTKULKTLAIGD TITSQELLAAQKILNKNGHPGYTIYERDSISVITHNDIDFRTILPMQOEFTYRVKNRQ AYINKKSGNEEINNTDLISKEYVLNKGKGPYDPDFRSHLKLFTIKYVDVDTNELL KSQSLTASRNEIDFRDYDPRQKALLYNNLDAFGIMDYTLTGKVEDNHDHDTNRIIT VYNGKPEGENASVHLAYDKDRYTEEREVYSYLRYGTGTPIDPNPNDK"
sig_peptide	819..896 /note="streptokinase signal peptide"
mat_peptide	897..2138 /product="streptokinase"

Alignment Scores:	
Pred. No.:	19.6
Score:	31.50
Percent Similarity:	48.00%
Best Local Similarity:	32.00%
Query Match:	5.02%
DB:	5
Gaps:	3
Indels:	9
Mismatches:	17
Conservative:	8
Matches:	16
Length:	2568

[illegible]

RESULT 20	EO3308	1262 bp	DNA	linear	PAT 29-SEP-1997
EO3308/c	DNA encoding recombinant streptokinase.				
LOCUS	EO3308				
DEFINITION	EO3308.1	GI:2171525			
ACCESSION	JP 1992011892-A/1.				
VERSION	synthetic construct				
KEYWORDS	synthetic construct				
SOURCE	artificial sequences.				
ORGANISM	1 (bases 1 to 1262)				
REFERENCE	Fujii, S., Katano, T., Majima, E., Ogino, K., Ono, K., Sakata, Y. and				
AUTHORS	Uenoyama, T.				
TITLE	PROTEIN OF STREPTOKINASES, CORRESPONDING GENE, CORRESPONDING PLASMID RECOMBINANT, CORRESPONDING CHARACTER TRANSFORMANT AND PRODUCTION				
JOURNAL	Patent: JP 1992011892-A 1 16-JAN-1992;				
COMMENT	OTSUKA PHARMACEUT FACTORY INC				
	OS Artificial gene				
	OC Artificial sequence; Genes.				
	PN JP 1992011892-A/1				
	PD 16-JAN-1992				

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PF    06-JUL-1990 JP 1980179851
PR   11-JUL-1989 JP 89P 179432, 27-NOV-1989 JP 89P 307957, PR
11-APR-1990 JP 90P 96830
PI FUJII SETSUO, KATANO TAMITAKA, MAJIMA EIJI, OGINO KOICHI, PI
ONO KENJI.
PI SAKATA YASUYO, UENOYAMA TSUTOMU
PC C12N15/58,C12N1/21,C12N9/70,(C12N1/21,C12R1:19),(C12N9/70, PC
C12R1:19);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: clone=pSKX;
FH Key Location/Qualifiers
FT      5'UTR          1..11
FT      CDS           12..1256
                        /product='recombinant streptokinase' FT
FT mat_peptide       12..1253
                       /product='recombinant streptokinase' FT
FT                                     1257..1263.
3'UTR                Location/Qualifiers
                         1..1262
                           /organism='synthetic construct'
                             /mol_type='genomic DNA'
                               /db_xref='taxon:32630'

FEATURES             source
Alignment Scores:
Pred. No.:         20            Length:        1262
Score:              27.00        Matches:         13
Percent Similarity: 44.44%     Conservative:    3
Best Local Similarity: 36.11%  Mismatches:        16
Query Match:        4.31%      Indels:           4
DB:                  Gaps:            2

US-09-940-235-4 (1-259) x E03308 (1-1262)
Qy    221 ArgGlyAsnLeuIeuGlnCysIleCysThr---GlyAsnGLyArgGlyGlu----- 236
||| ||| |
Db    188 CGGGGCAGGCCCTGTTCGGTTTACCACCATGGCGCGACGAGAGTGCAAGTCGAATTTC 129
||||| :|||
Qy    237 TriplycSGluArqHisrSerValGlInThrsSrGlyser 252
||| ||| |||
Db    128 GA AAAATTTCAGAGAGATGTCTCGTTAGTAGCTTCAAACAGTGCCAGC 81
||| ||| |||

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Search completed: December 6, 2004, 15:02:22
Job time : 6 secs

RESULT 1
 AAY24797
 ID AAY24797 standard; protein; 795 AA.
 XX

DT	16-NOV-1994	(first entry)
XX		
XX	Streptokinase.	
XX		
KW	Streptokinase; SK; Streptococcus equisimilis; plasminogen;	
KW	myocardial infarction.	
XX		
XX	Streptococcus dysgalactiae subsp. equisimilis.	
OS		
XX		
XX	Key	Location/Qualifiers
FT	Region	1. .352
FT		/note= "claim 3, see CC"
FT	Region	14. .414
FT		/note= "claim 1, see Cc"
FT	Region	120. .352
FT		/note= "claim 3, see CC"
FT	Region	244. .414
FT		/note= "claim 3, see CC"
FT	Region	244. .352
FT		/note= "claim 2, see CC"
XX	WO9407992-A1.	
PN		
XX		
XX	14-APR-1994.	
PD		
XX		
XX	05-OCT-1993;	93WO-US009502.
PF		
XX		
XX	05-OCT-1992;	92US-00956692.
PR		
XX	23-SEP-1993;	93US-00128299.
PR		
XX		
XX	(GEO) GEN HOSPITAL CORP.	
PA	(HARD) HARVARD COLLEGE.	
PA		
XX		
XX	Reed GL;	
PI		
XX		
XX	WPI; 1994-135561/16.	
DR		
XX		
PT	DNA encoding a polypeptide which binds to plasminogen and corresponds to	
PT	region of streptokinase - useful to detect plasminogen in a sample and to	
PT	treat myocardial infarction.	
PT		
XX		
PS	Disclosure; Page 40-41; 62pp; English.	
FS		
XX		
CC	Nucleic acid comprising a sequence encoding amino acids 14-414 of	
CC	streptokinase, which binds to plasminogen and does not have a sequence	
CC	comprising amino acids 60-414 is new. The polypeptide pref. comprises	
CC	amino acids 244-352, 1-352, 120-352 or 244-414. (Updated on 25-MAR-2003	
CC	to correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)	
XX		
SQ	Sequence 414 AA;	
	Query Match	5.0%; Score 31.5; DB 2; Length 414;
	Best Local Similarity	32.8%; Pred. No. 7.6;
	Matches	16; Conservative 8; Mismatches 17; Indels 9; Gaps 3;
QY	203 QDTR--TSYRIGTWSKDNRGNLL---QCICTGNRGKGEWKCRHTSVQT 247	
	::::: : : :: :	
Db	180 KDTKLKLTALGTTISQE---LLAQASILNKNHPGYTIYERDSSIVT 225	
	:: : : : :: :	
RESULT 5		
AAW94664		
ID	AAW94664 standard; protein; 414 AA.	
XX		
AC	AAW94664;	
XX		
XX	17-OCT-2003 (revised)	
DT		
DT	04-MAY-1999 (first entry)	
XX		
XX	Streptococcus equisimilis native streptokinase.	
XX		
XX	Streptococcus equisimilis H46A; streptokinase; mutant; fibrinolytic;	
KW	plasma clot; hydrolysis; haemolytic Streptococcus; plasminogen; plasmin;	

W09909698-A1

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PS Claim 30; Page 60-61; 73pp; English.
XX The present invention describes an isolated bacterial protein that
CC induces fibrin-dependent plasminogen activation in a pharmaceutical
CC composition for dissolving blood clots. Also described are: (1) a
CC composition comprising an isolated modified streptokinase, the
CC modification being removal of amino acid residues in the amino terminus;
CC (2) a method for dissolving a blood clot in a subject, comprising
CC administering to the subject a fibrin-dependent streptokinase protein; a
CC nucleic acid (1) encoding a modified bacterial streptokinase; (3) an
CC expression vector comprising (1); and (4) a host cell transformed with
CC the expression vector of (3). The pharmaceutical composition comprising a
CC bacterial fibrin-dependent plasminogen activator is useful for dissolving
CC blood clots in patients with a thrombotic condition, e.g. myocardial
CC infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis,
CC graft thrombosis and arterial thrombosis. The modified streptokinase can
CC also be used in non-human mammals. Streptokinase activation of
CC plasminogen is at least 10-fold, preferably 100-fold greater in the
CC presence of fibrin than in the absence of fibrin. The modified
CC streptokinase has at least one amino acid substitution that inactivates a
CC substrate site for proteolytic cleavage. This reduces the rate of
CC degradation of the streptokinase at least two-fold. The present sequence
CC represents native streptokinase (nSK). (Updated on 17-OCT-2003 to
XX standardise OS field)
SQ Sequence 414 AA;

Query Match          5.0%; Score 31.5; DB 5; Length 414;
Best Local Similarity 32.0%; Pred. No. 7.6;
Matches 16; Conservative 8; Mismatches 17; Indels 9; Gaps 3;

QY 203 QDTR--TSYRIGTWSKNGRNL---QCICGTNGRGWKCRHTSVQT 247
Db 180 KTKLKLTLAIGDTITSQE---LLAQASILNKNHPGYTIYERDSSIVT 225

RESULT 8
pct-us93-09502-1

Query Match          5.0%; Score 31.5; DB 7; Length 414;
Best Local Similarity 32.0%; Pred. No. 7.6;
Matches 16; Conservative 8; Mismatches 17; Indels 9; Gaps 3;

QY 203 QDTR--TSYRIGTWSKNGRNL---QCICGTNGRGWKCRHTSVQT 247
Db 180 KTKLKLTLAIGDTITSQE---LLAQASILNKNHPGYTIYERDSSIVT 225

RESULT 9
us-08-128-299-1

Query Match          5.0%; Score 31.5; DB 8; Length 414;
Best Local Similarity 32.0%; Pred. No. 7.6;
Matches 16; Conservative 8; Mismatches 17; Indels 9; Gaps 3;

QY 203 QDTR--TSYRIGTWSKNGRNL---QCICGTNGRGWKCRHTSVQT 247
Db 180 KTKLKLTLAIGDTITSQE---LLAQASILNKNHPGYTIYERDSSIVT 225

RESULT 10
us-09-211-542a-6

Query Match          5.0%; Score 31.5; DB 10; Length 414;
Best Local Similarity 32.0%; Pred. No. 7.6;
Matches 16; Conservative 8; Mismatches 17; Indels 9; Gaps 3;

QY 203 QDTR--TSYRIGTWSKNGRNL---QCICGTNGRGWKCRHTSVQT 247
Db 180 KTKLKLTLAIGDTITSQE---LLAQASILNKNHPGYTIYERDSSIVT 225

RESULT 11
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STRP_STRSQ
ID STRP_STRSQ STANDARD; PRT; 440 AA.
AC P00779;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Streptokinase C precursor.
GN Name=sk;
OS Streptococcus equisimilis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=119602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H46A;
RX MEDLINE=85232082; PubMed=2989113;
RA Malke H., Roe B., Ferretti J.J.;
RT "Nucleotide sequence of the streptokinase gene from Streptococcus
RL equisimilis H46A.";
RN [2]
RP SEQUENCE OF 27-440.
RX MEDLINE=83127125; PubMed=6760891;
RA Jackson K.W., Tang J.;
RT "Complete amino acid sequence of streptokinase and its homology with
RL serine proteases.";
RN [3]
RP BIOCHEMISTRY 21:6620-6625(1982).
CC -1- FUNCTION: This protein is not a protease, but it activates
CC plasminogen by complexing with it. As a potential virulence
CC factor, it is thought to prevent the formation of effective fibrin
CC barriers around the site of infection, thereby contributing to the
CC invasiveness of the cells.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC EMBL; X72832; CAA51351.1; -.
CC PIR; A00967; BZSO.
CC PIR; A22801; A22801.
CC PDB; 1L4D; X-ray; B=40-173.
CC PDB; 1L4Z; X-ray; B=26-173.
CC InterPro; IPR004093; Staphylokinase.
CC InterPro; IPR008124; Streptokinase.
CC Pfam; PF02821; Staphylokinase; 3.
CC PRINTS; PR01753; STREPKINASE.
CC 3D-structure; Direct protein sequencing; Plasminogen activation;
CC Signal; Virulence.
CC SIGNAL 1 26
CC CHAIN 27 440 Streptokinase C.
CC VARIANT 195 195 L -> D.
CC VARIANT 207 207 D -> L.
CC CONFLICT 298 300 EKY -> LEYK (in Ref. 2).
CC CONFLICT 438 438 N -> D (in Ref. 2).
CC STRAND 180 180
CC STRAND 184 194
CC TURN 199 200
CC TURN 203 204
CC STRAND 205 205
CC STRAND 209 214
CC TURN 216 217
CC STRAND 219 221
CC HELIX 222 236
CC TURN 238 239
CC STRAND 240 252
CC TURN 253 254
CC STRAND 259 260
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